

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 12:33:12 ; Search time 181 Seconds
(without alignments)
1788.500 Million cell updates/sec

Title: US-09-634-287E-2

Perfect score: 4570
Sequence: 1 MSQTSHPGRGLAGRWLNGA.....LHRAQILEILRRRPWAGRK 837

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04: *
1: Geneseqp1980s: *
2: Geneseqp1990s: *
3: Geneseqp2000s: *
4: Geneseqp2001s: *
5: Geneseqp2002s: *
6: Geneseqp2003as: *
7: Geneseqp2003bs: *
8: Geneseqp2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4570	100.0	837	2 AAW75425	Aaw75425 Human agg
2	4570	100.0	837	7 ADJ69542	Adj69542 Human hea
3	4570	100.0	837	8 ADS20209	Ads20209 Human agg
4	4567	99.9	846	8 ADS20232	Ads20232 Human agg
5	4566	99.9	837	4 AAG78228	Aag78228 Human agg
6	4566	99.9	837	7 ADB85488	Adb85488 Human agg
7	4566	99.9	840	3 AAB21256	Aab21256 Human met
8	4563	99.8	837	3 AAY99429	Aay99429 Human PRO
9	4563	99.8	837	4 AAB66178	Aab66178 Protein o
10	4563	99.8	837	4 AAU29199	Aau29199 Human PRO
11	4563	99.8	837	6 ABUS58575	Abu58575 Human PRO
12	4563	99.8	837	6 ABU88123	Abu88123 Novel hum
13	4563	99.8	837	6 ABU84438	Abu84438 Human sec
14	4563	99.8	837	6 ABR66312	Abr66312 Human sec
15	4563	99.8	837	6 ABR65702	Abr65702 Human sec
16	4563	99.8	837	6 ABU99642	Abu99642 Human sec
17	4563	99.8	837	6 ABU82881	Abu82881 Human PRO
18	4563	99.8	837	6 ABU90002	Abu90002 Novel hum
19	4563	99.8	837	6 ABR68251	Abr68251 Human sec
20	4563	99.8	837	6 ABR96304	Abr96304 Novel hum
21	4563	99.8	837	6 ABU92735	Abu92735 Human sec
22	4563	99.8	837	6 ABO08812	Abo08812 Human sec
23	4563	99.8	837	6 ABO02864	Abo02864 Human sec
24	4563	99.8	837	6 ABR75018	Abr75018 Human sec
25	4563	99.8	837	6 ABR94780	Abr94780 Human sec

26	4563	99.8	837	6 ABU85753	Abu85753 Human PRO
27	4563	99.8	837	6 ABU98913	Abu98913 Novel hum
28	4563	99.8	837	6 ABU98128	Abu98128 Novel hum
29	4563	99.8	837	6 ABU91834	Abu91834 Novel hum
30	4563	99.8	837	6 ABU89527	Abu89527 Human PRO
31	4563	99.8	837	6 ABU86368	Abu86368 Human sec
32	4563	99.8	837	6 ABU67581	Abu67581 Human PRO
33	4563	99.8	837	6 ABU80609	Abu80609 Human PRO
34	4563	99.8	837	6 ABR99527	Abr99527 Human sec
35	4563	99.8	837	6 ABR98917	Abr98917 Human sec
36	4563	99.8	837	6 ABO16440	Abo16440 Human sec
37	4563	99.8	837	6 ABR92340	Abr92340 Human sec
38	4563	99.8	837	6 ABO18981	Abo18981 Human sec
39	4563	99.8	837	6 ABR78402	Abr78402 Human sec
40	4563	99.8	837	6 ABU85138	Abu85138 Novel hum
41	4563	99.8	837	6 ABO00277	Abo00277 Novel hum
42	4563	99.8	837	6 ABO11609	Abo11609 Human sec
43	4563	99.8	837	6 ABO02254	Abo02254 Human sec
44	4563	99.8	837	6 ABU88828	Abu88828 Novel hum
45	4563	99.8	837	6 ABU83523	Abu83523 Human sec

ALIGNMENTS

RESULT 1
AAW75425
ID AAW75425 standard; protein; 837 AA.
XX AC AAW75425;
XX DT 30-MAR-1999 (first entry)
XX DE Human aggrecan degrading metalloprotease 1.
XX KW Human; aggrecan degrading metalloprotease; cartilage; proteoglycan;
KW interglobular domain; matrix metalloprotease; bovine; interleukin-1beta;
KW primer; PCR; amplification; inhibitor; cleavage; inhibitor; ADMP;
KW arthritis; joint injury; pseudogout.
XX OS Homo sapiens.
XX PN WO9905291-A2.
XX PD 04-FEB-1999.
XX PF 24-JUL-1998; 98WO-US015438.
XX PR 25-JUL-1997; 97US-0053850P.
PR 15-AUG-1997; 97US-0055836P.
PR 16-OCT-1997; 97US-0062169P.
PA (DUPO) DU PONT PHARM CO.
PI Arner EC, Burn TC, Copeland RA, Decicco CP, Liu R, Magolda R;
PI Pratta M, Solomon KA, Tortorella MD, Trzaskos JW, Yang F;
XX WPI: 1999-142943/12.
DR N-PSDB; AAX00725.
XX New isolated aggrecan degrading metallo proteases - used to develop
products for treating, e.g. osteoarthritis, joint injury, reactive
arthritis, psoriatic arthritis or juvenile rheumatoid arthritis.
PS Claim 25; Page 61-62; 73pp; English.
XX This sequence represents the human aggrecan degrading metalloprotease 1
(ADMP-1). ADMP-1 and ADMP-2 (AAW75426) are novel proteases that cleave
the aggrecan (a major cartilage proteoglycan) between residues Glu373-
Ala374 of the interglobular domain (compared with cleavage between Asn341
-Phe342 by the matrix metalloproteases MMP-1, -2, -3, -7, -8, -9 and -
13). ADMP-1 and ADMP-2 were isolated and purified from the conditioned
media of bovine nasal cartilage stimulated by interleukin-1beta. The

CC purified proteins were partially sequenced and primers were synthesised
 CC based on the resultant amino acid sequences (AA00727-X00732 for ADMP-1
 CC and AA00733-X00736 for ADMP-2). These were used to isolate the
 CC corresponding genes from cDNA. The ADMP polypeptides can be used for
 CC identifying inhibitors of ADMP activity which would prevent cleavage of
 CC the aggrecan core protein, thereby decreasing the loss of aggrecan from
 CC cartilage. Such inhibitors can be used for treating diseases such as
 CC osteoarthritis, joint injury, reactive arthritis, acute pyrophosphate
 CC arthritis (pseudogout), psoriatic arthritis and juvenile rheumatoid
 CC arthritis
 XX
 SQ Sequence 837 AA;

Query Match 100.0%; Score 4570; DB 2; Length 837;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 837; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSQTGSHPGRLAGRWLWGAQPCLLPIVPLSLWMLLLILLASLLPSARLASPLPREEE 60
 DB 1 MSQTGSHPGRLAGRWLWGAQPCLLPIVPLSLWMLLLILLASLLPSARLASPLPREEE 60
 QY 61 IVFPEKINGSVLPFGSGAPARLLCRLOAFGETLLEQDSGVQVEGLTVQYLQAPPELLG 120
 DB 61 IVFPEKINGSVLPFGSGAPARLLCRLOAFGETLLEQDSGVQVEGLTVQYLQAPPELLG 120
 QY 121 GAEPGYLTGTINGDPESVASLHWDGALIGVLYRGAEHLQPLRGSTPNSAGGPGAH 180
 DB 121 GAEPGYLTGTINGDPESVASLHWDGALIGVLYRGAEHLQPLRGSTPNSAGGPGAH 180
 QY 181 LRKSPASGGGPNKCNKAPLGSPPRRAKRPAFLSRFVETLVVADDDKMAAFHAGLKR 240
 DB 181 LRKSPASGGGPNKCNKAPLGSPPRRAKRPAFLSRFVETLVVADDDKMAAFHAGLKR 240
 QY 241 YLTVMAAAAKAFKPIRNPVSLVTRVLVILSGEGEPQVGPSSAAQTLSFCWQORGLN 300
 DB 241 YLTVMAAAAKAFKPIRNPVSLVTRVLVILSGEGEPQVGPSSAAQTLSFCWQORGLN 300
 QY 301 TPEDSDPDHEDTALLFTRODLGVSTCDTLGMADVGTVCDDPARSCAIVDDGLOSAFTAA 360
 DB 301 TPEDSDPDHEDTALLFTRODLGVSTCDTLGMADVGTVCDDPARSCAIVDDGLOSAFTAA 360
 QY 361 HELGHVFNMLHDSKPCISLNGPLSTSRHYWAPVMAHVDPEEPWSPCSARFIFDLDNGY 420
 DB 361 HELGHVFNMLHDSKPCISLNGPLSTSRHYWAPVMAHVDPEEPWSPCSARFIFDLDNGY 420
 QY 421 GHCLLDKPEAPLHLVTPFGKYDADRQCQLTFGPDSSRHCPQLPPCAALWCSGHLNGHA 480
 DB 421 GHCLLDKPEAPLHLVTPFGKYDADRQCQLTFGPDSSRHCPQLPPCAALWCSGHLNGHA 480
 QY 481 MCQTKHSPWADGTPCGPAQACMGRCILHMDLODENIPOAGGWPWGPWGDSCSRTCGGV 540
 DB 481 MCQTKHSPWADGTPCGPAQACMGRCILHMDLODENIPOAGGWPWGPWGDSCSRTCGGV 540
 QY 541 QFSRDCRTPVPRNGKYGCEGRTRFRSCNTEBCTGSAITFEEOCAAYNHRTDLFKSF 600
 DB 541 QFSRDCRTPVPRNGKYGCEGRTRFRSCNTEBCTGSAITFEEOCAAYNHRTDLFKSF 600
 QY 601 FGPMDWVPRTYGVAPQDCKLTQARALGYVYVLEPRVVDGTPCSPDSSVCVQGRCIHA 660
 DB 601 FGPMDWVPRTYGVAPQDCKLTQARALGYVYVLEPRVVDGTPCSPDSSVCVQGRCIHA 660
 QY 661 GCDRIIGSKKKFKDKMVCVGGSGCSKQSGFRKRYGYNVVTIPAGATHILVROQGNP 720
 DB 661 GCDRIIGSKKKFKDKMVCVGGSGCSKQSGFRKRYGYNVVTIPAGATHILVROQGNP 720
 QY 721 GHSIYLALKLPDGSYALNGEYTLMPSTDVLPFGAVSLRYSGATASETLSHGGLAQP 780
 DB 721 GHSIYLALKLPDGSYALNGEYTLMPSTDVLPFGAVSLRYSGATASETLSHGGLAQP 780
 QY 781 LTLQVLVAGNPQDTRLRYSPFVRPTSTPRPTQDMLHRRRAQILEILRRRPPWAGRK 837
 DB 781 LTLQVLVAGNPQDTRLRYSPFVRPTSTPRPTQDMLHRRRAQILEILRRRPPWAGRK 837

RESULT 2
 ADJ69542
 ID ADJ69542 standard; protein; 837 AA.
 AC ADJ69542;
 DT 06-MAY-2004 (first entry)
 XX Human heat mitochondrial protein as a therapeutic target SeqID1348.
 DE
 KW mitochondrial; human; screening assay; diabetes mellitus;
 KW Huntington's disease; osteoarthritis;
 KW Leber's hereditary optic neuropathy; LHON;
 KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
 KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
 KW neuroprotective; nontropic; antidiabetic; anticonvulsant; antiarthritic;
 KW osteopathic; ophthalmological; cytostatic.
 OS Homo sapiens.
 XX
 PN WO2003087768-A2.
 XX
 PD 23-OCT-2003.
 XX
 PF 04-APR-2003; 2003WO-US010870.
 XX
 PR 12-APR-2002; 2002US-0372843P.
 PR 17-JUN-2002; 2002US-0389987P.
 PR 20-SEP-2002; 2002US-0412418P.
 XX
 PA (MITO-) MITOKOR.
 PA (BUCK-) BUCK INST AGE RES.
 XX
 PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
 PI Warnock DE;
 XX
 DR WPI; 2003-845369/78.
 XX
 PT Identifying a mitochondrial target for drug screening assays and for
 PT treating diseases associated with altered mitochondrial function,
 PT comprises detecting a modified polypeptide in a sample and correlating
 PT with the disease.
 XX
 PS Claim 1; SEQ ID NO 1348; 180pp; English.
 XX
 CC This invention relates to novel mitochondrial targets that can be used
 CC for therapeutic intervention in treating a disease associated with
 CC altered mitochondrial function. Specifically, it refers to a method for
 CC identifying proteins of the human heart mitochondrial proteome that are
 CC useful for drug screening assays, as well as therapeutic targets. The
 CC present invention describes a method for identifying such proteins that
 CC can be used in the treatment of various diseases associated with altered
 CC mitochondrial function including diabetes mellitus, Huntington's disease,
 CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
 CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
 CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
 CC compositions have neuroprotective, nontropic, antidiabetic,
 CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
 CC cytostatic activities. This polypeptide sequence is a human heart
 CC mitochondrial protein of the invention.
 XX
 SQ Sequence 837 AA;

Query Match 100.0%; Score 4570; DB 7; Length 837;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 837; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSQTGSHPGRLAGRWLWGAQPCLLPIVPLSLWMLLLILLASLLPSARLASPLPREEE 60
 DB 1 MSQTGSHPGRLAGRWLWGAQPCLLPIVPLSLWMLLLILLASLLPSARLASPLPREEE 60
 QY 61 IVFPEKINGSVLPFGSGAPARLLCRLOAFGETLLEQDSGVQVEGLTVQYLQAPPELLG 120

Db 61 IVPPEKLSVLPFGSGAPARLLCRLOAFGETLLLEQDSGVQVEGLTVQYLGAPELIG 120
QY 121 GAEPGYLTGTINGDPESVASLHWDGALLGVLYRGAEHLQPLEGGTPNSAGPGAH 180
Db 121 GAEPGYLTGTINGDPESVASLHWDGALLGVLYRGAEHLQPLEGGTPNSAGPGAH 180
QY 181 LRKSPASGGPWCNVKAPLPGSPSPRRPRAKRPAFLSRFVETLVVADDDKAAAFHGAGLKR 240
Db 181 LRKSPASGGPWCNVKAPLPGSPSPRRPRAKRPAFLSRFVETLVVADDDKAAAFHGAGLKR 240
QY 241 YLLTWMAAAKAFKPSIRNPVSLVTRVLVILSGEGPQVGSAAQTLSFCAWORGLN 300
Db 241 YLLTWMAAAKAFKPSIRNPVSLVTRVLVILSGEGPQVGSAAQTLSFCAWORGLN 300
QY 301 TPEDSDPHDFTAILFTRODLGVSTCDTLGHADVGTCDPARSCAIVEDDGLQSAFTAA 360
Db 301 TPEDSDPHDFTAILFTRODLGVSTCDTLGHADVGTCDPARSCAIVEDDGLQSAFTAA 360
QY 361 HELGHVFNMLHNSKPCISLNGPLSTSRHVMAFVMAHVDPEPWPSPCSARFITDFLDNGY 420
Db 361 HELGHVFNMLHNSKPCISLNGPLSTSRHVMAFVMAHVDPEPWPSPCSARFITDFLDNGY 420
QY 421 GHCLLDKPEAPLHLVPTFGKYDADRCQLTFGPDSDRHCPOLPDPPCAALWCSGHLNGHA 480
Db 421 GHCLLDKPEAPLHLVPTFGKYDADRCQLTFGPDSDRHCPOLPDPPCAALWCSGHLNGHA 480
QY 481 MCQTKHSPWADGTPCGPAQACMGRCCLHMDQLQDFNIPOAGGWPMPGDCSRTCGGV 540
Db 481 MCQTKHSPWADGTPCGPAQACMGRCCLHMDQLQDFNIPOAGGWPMPGDCSRTCGGV 540
QY 541 QFSRDCTRPVPRNGSKYCEGRTRFRSCNTEDCPTGSALTFRBQCAAYNHRITLFSKF 600
Db 541 QFSRDCTRPVPRNGSKYCEGRTRFRSCNTEDCPTGSALTFRBQCAAYNHRITLFSKF 600
QY 601 PGPMWVPRYTGVAPQDQCKLTCOARALGYVYVLEPRVVDGTPCPDSSVVCQGRCIHA 660
Db 601 PGPMWVPRYTGVAPQDQCKLTCOARALGYVYVLEPRVVDGTPCPDSSVVCQGRCIHA 660
QY 661 GCDRIIGSKKFDKCMVCGDGGSGSKSGSKPRKRYGNNVVTIPAGATHILVQQGNP 720
Db 661 GCDRIIGSKKFDKCMVCGDGGSGSKSGSKPRKRYGNNVVTIPAGATHILVQQGNP 720
QY 721 GHSIYVLAALPDGSGYALNGEYTLMPSTDDVVLPGAVSLRYSYGATAAETLSHGGLAQP 780
Db 721 GHSIYVLAALPDGSGYALNGEYTLMPSTDDVVLPGAVSLRYSYGATAAETLSHGGLAQP 780
QY 781 LTQLVLVAGNPQDRLRYSFVPRPTPPTPQDHLHRAQILEILRRRPPWAGRK 837
Db 781 LTQLVLVAGNPQDRLRYSFVPRPTPPTPQDHLHRAQILEILRRRPPWAGRK 837

RESULT 3

ADS20209
ID ADS20209 standard; protein; 837 AA.
XX AC ADS20209;
XX DT 18-NOV-2004 (first entry)
XX DE Human aggrecanase ADAMTS4 pro-protein.
XX KW ADAMTS4; a disintegrin-like and metalloprotease;
KW thrombospondin type 1 motif 4; reprotysin; zinc metalloprotease;
KW aggrecanase; osteoarthritis; antiinflammatory; antiarthritic; antirheumatic;
KW cytostatic; osteoarthritis; glioma; cancer; inflammatory joint;
KW rheumatoid arthritis; septic arthritis; periodontal; Crohn's disease;
KW human; pro-protein; chromosome 1q21-q23; enzyme.
OS Homo sapiens.
XX Key Location/Qualifiers
FH 1. .212
FT Peptide

Query Match 100.0%; Score 4570; DB 8; Length 837;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 837; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSQTGSHPGRLAGRWLWGAQPCLLLPVPLSWLVWLLLLASLLPSARLASPLPREE 60
QY 1 MSQTGSHPGRLAGRWLWGAQPCLLLPVPLSWLVWLLLLASLLPSARLASPLPREE 60
Db 61 IVPPEKLSVLPFGSGAPARLLCRLOAFGETLLLEQDSGVQVEGLTVQYLGAPELIG 120
Db 61 IVPPEKLSVLPFGSGAPARLLCRLOAFGETLLLEQDSGVQVEGLTVQYLGAPELIG 120

FT Domain /note= "Pro-peptide"
FT 213. .436
FT /note = Metalloprotease catalytic domain
FT 437. .519
FT /note = Disintegrin-like domain
FT 520. .576
FT /note = TSP-1 (thrombospondin type I) motif
FT 577. .685
FT /note = Cysteine-rich domain
FT 581. .582
FT /note= "Auto-digestion cleavage site"
FT 686. .837
FT /note = Spacer domain
FT 694. .695
FT /note= "Auto-digestion cleavage site"

W02004011637-A2.

05-FEB-2004.

29-JUL-2003; 2003WO-US023484.

29-JUL-2002; 2002US-0398721P.

(AMHP) WYETH.

(CORC/) CORCORAN C J.

(FLAN/) FLANNERY C R.

(ZENG/) ZENG W.

(RACI/) RACIE L A.

(MCD/) MCDONAGH T.

(FREE/) FREEMAN B A.

(GEOR/) GEORGIADIS K E.

(LAVA/) LAVALLIE B R.

Corcoran CJ, Flannery CR, Zeng W, Racie LA, Mcdonagh T;

Freeman BA, Georgiadis KE, Lavallie ER;

WPI; 2004-143860/14.

New isolated, modified ADAMTS4 (aggrecanase) protein with improved stability useful for identifying inhibitors of the enzyme activity for treating aggrecanase-associated conditions, including osteoarthritis.

Example 6; SEQ ID NO 1; 117pp; English.

The invention relates to a novel isolated, modified ADAMTS4 (a

disintegrin-like and metalloprotease (reprotysin type) with

thrombospondin type 1 motif 4) protein with improved stability compared

to a naturally occurring, full-length ADAMTS4 protein, where the modified

protein differs from the naturally-occurring, full-length ADAMTS4 protein

by at least one amino acid. ADAMTS proteins are a subfamily of zinc

metalloproteases and include aggrecanases amongst their members. The

protein of the invention demonstrates osteopathic, antiinflammatory,

antiarthritic, antirheumatic and cytostatic activities and may be useful

for treating aggrecanase-associated conditions, including osteoarthritis,

glioma, cancer, inflammatory joint disease, rheumatoid arthritis, septic

arthritis, periodontal disease and Crohn's disease. The current sequence

is that of the human aggrecanase ADAMTS4 pro-protein of the invention

which is encoded by DNA located at chromosome 1q21-q23.

Sequence 837 AA;

121 GABPGYLTGTINGDPEVASLHWDGALLGVLYRGAEHLQPLEGGTNSAGGCAHI 180
 121 GABPGYLTGTINGDPEVASLHWDGALLGVLYRGAEHLQPLEGGTNSAGGCAHI 180
 181 LRKSPASGOGMNCVKAPLGSPSPRPRAKRPFASLRFVETLVVADDDKMAAFHAGLKR 240
 181 LRKSPASGOGMNCVKAPLGSPSPRPRAKRPFASLRFVETLVVADDDKMAAFHAGLKR 240
 241 YLLTVMMAAAKAFKHPISIRNPVSLVTRVLVILSGEGEPQVGSAAQTILRSFCWQORGLN 300
 241 YLLTVMMAAAKAFKHPISIRNPVSLVTRVLVILSGEGEPQVGSAAQTILRSFCWQORGLN 300
 301 TPDSDPDHPDTHAILTRQDLQGVSTCDTLGMADVTCVCDPARSCAIVDDGLQSAFTAA 360
 301 TPDSDPDHPDTHAILTRQDLQGVSTCDTLGMADVTCVCDPARSCAIVDDGLQSAFTAA 360
 361 HELGHVFNMLHDSKPCISLNGPLSTSRHVMAPVMAHVDPEEPWSPCSARFITDFLDNGY 420
 361 HELGHVFNMLHDSKPCISLNGPLSTSRHVMAPVMAHVDPEEPWSPCSARFITDFLDNGY 420
 421 GHCLLDKPEAPLHLPVTFPGKYDADRQCQLTFGPDSPHCPQLPPPCAALMCSGHLNGHA 480
 421 GHCLLDKPEAPLHLPVTFPGKYDADRQCQLTFGPDSPHCPQLPPPCAALMCSGHLNGHA 480
 481 MCQTKSPWADGTPCGPAQACMGRCCLHMDLODFNIPOAGGWGMPGWDGCSRTCGGV 540
 481 MCQTKSPWADGTPCGPAQACMGRCCLHMDLODFNIPOAGGWGMPGWDGCSRTCGGV 540
 541 QFSRDCTRPVPRNGGKCEGRTRFRSCNTEDCPTGSALTFRFEEQCAAYNHRITDLFKSF 600
 541 QFSRDCTRPVPRNGGKCEGRTRFRSCNTEDCPTGSALTFRFEEQCAAYNHRITDLFKSF 600
 601 PGPMWVPRVTGVAPOQCKLTQCARALGVYVYVLEPRVDGTGTPCSPDSSVCVQGRCHIA 660
 601 PGPMWVPRVTGVAPOQCKLTQCARALGVYVYVLEPRVDGTGTPCSPDSSVCVQGRCHIA 660
 661 GCDRIITGKKKFKDKMVCWGDSGSCSKSGSPRFRGYNNVVTIPAGATHILVROQGNP 720
 661 GCDRIITGKKKFKDKMVCWGDSGSCSKSGSPRFRGYNNVVTIPAGATHILVROQGNP 720
 721 GHSIYLAALKLPDGSYALNGEYTIMPSPTDVLPGAVSLRYSGATAASETLSHGFLAQP 780
 721 GHSIYLAALKLPDGSYALNGEYTIMPSPTDVLPGAVSLRYSGATAASETLSHGFLAQP 780
 781 LTLQVLVAGNPQDTRLYSFVPRPTSTPRTPQDWLHRAQILTEILRRPWAGRK 837
 781 LTLQVLVAGNPQDTRLYSFVPRPTSTPRTPQDWLHRAQILTEILRRPWAGRK 837

RESULT 4
 ADS20232
 ID ADS20232 standard; protein; 846 AA.
 AC XX
 AC XX
 AC XX
 DT 18-NOV-2004 (first entry)
 DX XX
 DE XX
 DE XX
 KW XX
 KW XX
 KW XX
 KW XX
 KW XX
 KW XX
 OS Homo sapiens.
 OS Synthetic.
 XX Key Location/Qualifiers
 FH Misc-difference 362
 FT /note= "Wild-type Glu substituted by Gln"

Misc-difference 838. .846
 /note= "FLAG tag"
 WO2004011637-A2.
 05-FEB-2004.
 29-JUL-2003; 2003WO-US023484.
 29-JUL-2002; 2002US-0398721P.
 (AMHP) WYETH.
 (CORC/) CORCORAN C J.
 (FLAN/) FLANNERY C R.
 (ZENG/) ZENG W.
 (RACI/) RACIE L A.
 (MCDO/) MCDONAGH T.
 (FREE/) FREEMAN B A.
 (GEOR/) GEORGIADIS K E.
 (LAVA/) LAVALLIE E R.
 Corcoran CJ, Flannery CR, Zeng W, Racie LA, Mcdonagh T;
 Freeman BA, Georgiadis KE, Lavallie ER;
 WPI; 2004-143860/14.
 New isolated, modified ADAMTS4 (aggrecanase) protein with improved
 stability useful for identifying inhibitors of the enzyme activity for
 treating aggrecanase-associated conditions, including osteoarthritis.
 Claim 9; SEQ ID NO 29; 117pp; English.
 The invention relates to a novel isolated, modified ADAMTS4 (a
 disintegrin-like and metalloprotease (reprolysin type) with
 thrombospondin type 1 motif 4) protein with improved stability compared
 to a naturally occurring, full-length ADAMTS4 protein, where the modified
 protein differs from the naturally-occurring, full-length ADAMTS4 protein
 by at least one amino acid. ADAMTS proteins are a subfamily of zinc
 metalloproteases and include aggrecanases amongst their members. The
 protein of the invention demonstrates osteopathic, antiinflammatory,
 antiarthritic, anirheumatic and cytostatic activities and may be useful
 for treating aggrecanase-associated conditions, including osteoarthritis,
 glioma, cancer, inflammatory joint disease, rheumatoid arthritis, septic
 arthritis, periodontal disease and Crohn's disease. The current sequence
 is that of the human aggrecanase ADAMTS4 mutant E362Q protein with FLAG
 tag of the invention.
 Sequence 846 AA;
 Query Match 99.9%; Score 4567; DB 8; Length 846;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 836; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSQTGSHPGRLAGRWLWGAQPCLLPIVPLSLWMLLLLLASLPSARLASPLPREE 60
 DB 1 MSQTGSHPGRLAGRWLWGAQPCLLPIVPLSLWMLLLLLASLPSARLASPLPREE 60
 QY 61 IVFPEKLSVLPVPGSGAPARLLCRLQAFGETLLELEQDSGVQVEGLTVQYLGAPELIG 120
 DB 61 IVFPEKLSVLPVPGSGAPARLLCRLQAFGETLLELEQDSGVQVEGLTVQYLGAPELIG 120
 QY 121 GABPGYLTGTINGDPEVASLHWDGALLGVLYRGAEHLQPLEGGTNSAGGCAHI 180
 DB 121 GABPGYLTGTINGDPEVASLHWDGALLGVLYRGAEHLQPLEGGTNSAGGCAHI 180
 QY 181 LRKSPASGOGMNCVKAPLGSPSPRPRAKRPFASLRFVETLVVADDDKMAAFHAGLKR 240
 DB 181 LRKSPASGOGMNCVKAPLGSPSPRPRAKRPFASLRFVETLVVADDDKMAAFHAGLKR 240
 QY 241 YLLTVMMAAAKAFKHPISIRNPVSLVTRVLVILSGEGEPQVGSAAQTILRSFCWQORGLN 300
 DB 241 YLLTVMMAAAKAFKHPISIRNPVSLVTRVLVILSGEGEPQVGSAAQTILRSFCWQORGLN 300

QY 301 TPEDSDPHDFTAILFTRODLGVSTCDTLGNADVTCVCDPARSCAIVEDDGLQSAFTAA 360
 Db TPEDSDPHDFTAILFTRODLGVSTCDTLGNADVTCVCDPARSCAIVEDDGLQSAFTAA 360
 QY 361 HELGHVFNMLHNSKPCISLNGPLSTRSHVMAVPMVAHVDPPEPWPSCSARFITDFLDNGY 420
 Db HQHGHVFNMLHNSKPCISLNGPLSTRSHVMAVPMVAHVDPPEPWPSCSARFITDFLDNGY 420
 QY 421 GHCLLDKPEAPLHLVPTFFGKDYDADRCQLTFGPDPSRHCPCQLPPPCAALWCSGHLNGHA 480
 Db GHCLLDKPEAPLHLVPTFFGKDYDADRCQLTFGPDPSRHCPCQLPPPCAALWCSGHLNGHA 480
 QY 481 MCQTKHSPWADGTPCGPAQACMGGRCLHMDQLQDFNIPOAGGKMPGMPGDCSRTCCGGV 540
 Db MCQTKHSPWADGTPCGPAQACMGGRCLHMDQLQDFNIPOAGGKMPGMPGDCSRTCCGGV 540
 QY 541 QFSRRDCTRPVPRNGGKYCEGRTRFRSCNTEDCPTGSALTFRFEEQCAAYNHRITDLFKSF 600
 Db QFSRRDCTRPVPRNGGKYCEGRTRFRSCNTEDCPTGSALTFRFEEQCAAYNHRITDLFKSF 600
 QY 601 PGPMWVPRYTGVAPODQCKLTQARALGYVYVLEPRVVDGTPCSPDSSSVCVQGRCIHA 660
 Db PGPMWVPRYTGVAPODQCKLTQARALGYVYVLEPRVVDGTPCSPDSSSVCVQGRCIHA 660
 QY 661 GCDRIIGSKKFKDKCMVCGDGGSGCSKQSGSFRKFRYGYNNVVTIPAGATHILVROQGNP 720
 Db GCDRIIGSKKFKDKCMVCGDGGSGCSKQSGSFRKFRYGYNNVVTIPAGATHILVROQGNP 720
 QY 721 GHRISYLALKLPDGSYALNGEYTLMPSPDVLPGAVSLRYSGATAAETLSGHGCLAOP 780
 Db GHRISYLALKLPDGSYALNGEYTLMPSPDVLPGAVSLRYSGATAAETLSGHGCLAOP 780
 QY 781 LTLQVLVAGNPQDTRLRYSFVPRPTPTPQDMLHRRQAILEILRRRPWAGRK 837
 Db LTLQVLVAGNPQDTRLRYSFVPRPTPTPQDMLHRRQAILEILRRRPWAGRK 837

RESULT 5
 AAG78228

ID AAG78228 standard; protein; 837 AA.

XX AC AAG78228;

XX DT 13-DEC-2001 (first entry)

XX DE Human aggrecanase-1 SEQ ID NO 3.

XX KW Human; aggrecanase-1; ADAMTS4; promoter; antiarthritic.

XX OS Homo sapiens.

XX PN JP2001245663-A.

XX PD 11-SEP-2001.

XX PF 06-MAR-2000; 2000JP-00059952.

XX PR 06-MAR-2000; 2000JP-00059952.

XX PA (EISA) EISAI CO LTD.

XX DR WPI; 2001-610072/70.

XX DR N-PSDB; AAI68146.

XX PT New DNA for use as a promoter for controlling the expression of

XX PT aggrecanase-1.

XX PS Disclosure; Page 9-11; 12pp; Japanese.

XX CC The invention relates to a DNA acting as a promoter controlling the
 CC expression of aggrecanase-1 (ADAMTS4) resulting in antiarthritic
 CC activity. The DNA is used in a method for screening a compound affecting
 CC the expression control of the aggrecanase-1 gene

XX SQ Sequence 837 AA;

Query Match 99.9%; Score 4566; DB 4; Length 837;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 836; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSQTSQSHPGRLAGRLWLGQAQPCLLLPVPLSWLWMLLLLLASLLPSARLASPLPREE 60

Db 1 MSQTSQSHPGRLAGRLWLGQAQPCLLLPVPLSWLWMLLLLLASLLPSARLASPLPREE 60

QY 61 IVFPEKLNGSVLPSSGAPARLLCRLOAFGETLLLELQDSGVQVEGLTVQYLQAPPELLG 120

Db 61 IVFPEKLNGSVLPSSGAPARLLCRLOAFGETLLLELQDSGVQVEGLTVQYLQAPPELLG 120

QY 121 GAEPGTYLGTGTNGDPESVASLHWDGGLLVQVYRGAELHLOPLEGGTPNSAGGGAHI 180

Db 121 GAEPGTYLGTGTNGDPESVASLHWDGGLLVQVYRGAELHLOPLEGGTPNSAGGGAHI 180

QY 181 LRRKSPASQGGPMCNVKAFLGSPSPRRRAKRFASLSRFVETLVVADDDKMAAFHGAGLKR 240

Db 181 LRRKSPASQGGPMCNVKAFLGSPSPRRRAKRFASLSRFVETLVVADDDKMAAFHGAGLKR 240

QY 241 YLLTWAAAAAKAFKHPSTRNPVSLVTRILVILSGSEEGPQVGPAAQTURSPFCAMORGLN 300

Db 241 YLLTWAAAAAKAFKHPSTRNPVSLVTRILVILSGSEEGPQVGPAAQTURSPFCAMORGLN 300

QY 301 TPEDSDPHDFTAILFTRODLGVSTCDTLGNADVTCVCDPARSCAIVEDDGLQSAFTAA 360

Db 301 TPEDSDPHDFTAILFTRODLGVSTCDTLGNADVTCVCDPARSCAIVEDDGLQSAFTAA 360

QY 361 HELGHVFNMLHNSKPCISLNGPLSTRSHVMAVPMVAHVDPPEPWPSCSARFITDFLDNGY 420

Db 361 HELGHVFNMLHNSKPCISLNGPLSTRSHVMAVPMVAHVDPPEPWPSCSARFITDFLDNGY 420

QY 421 GHCLLDKPEAPLHLVPTFFGKDYDADRCQLTFGPDPSRHCPCQLPPPCAALWCSGHLNGHA 480

Db 421 GHCLLDKPEAPLHLVPTFFGKDYDADRCQLTFGPDPSRHCPCQLPPPCAALWCSGHLNGHA 480

QY 481 MCQTKHSPWADGTPCGPAQACMGGRCLHMDQLQDFNIPOAGGKMPGMPGDCSRTCCGGV 540

Db 481 MCQTKHSPWADGTPCGPAQACMGGRCLHMDQLQDFNIPOAGGKMPGMPGDCSRTCCGGV 540

QY 541 QFSRRDCTRPVPRNGGKYCEGRTRFRSCNTEDCPTGSALTFRFEEQCAAYNHRITDLFKSF 600

Db 541 QFSRRDCTRPVPRNGGKYCEGRTRFRSCNTEDCPTGSALTFRFEEQCAAYNHRITDLFKSF 600

QY 601 PGPMWVPRYTGVAPODQCKLTQARALGYVYVLEPRVVDGTPCSPDSSSVCVQGRCIHA 660

Db 601 PGPMWVPRYTGVAPODQCKLTQARALGYVYVLEPRVVDGTPCSPDSSSVCVQGRCIHA 660

QY 661 GCDRIIGSKKFKDKCMVCGDGGSGCSKQSGSFRKFRYGYNNVVTIPAGATHILVROQGNP 720

Db 661 GCDRIIGSKKFKDKCMVCGDGGSGCSKQSGSFRKFRYGYNNVVTIPAGATHILVROQGNP 720

QY 721 GHRISYLALKLPDGSYALNGEYTLMPSPDVLPGAVSLRYSGATAAETLSGHGCLAOP 780

Db 721 GHRISYLALKLPDGSYALNGEYTLMPSPDVLPGAVSLRYSGATAAETLSGHGCLAOP 780

QY 781 LTLQVLVAGNPQDTRLRYSFVPRPTPTPQDMLHRRQAILEILRRRPWAGRK 837

Db 781 LTLQVLVAGNPQDTRLRYSFVPRPTPTPQDMLHRRQAILEILRRRPWAGRK 837

RESULT 6
 ADB85488

ID ADB85488 standard; protein; 837 AA.

XX AC ADB85488;

XX DT 04-DEC-2003 (first entry)

XX DE Human aggrecanase-1 (ADAMTS-4) wild-type protein sequence.

XX KW aggrecanase; aggrecan; articular cartilage; proteoglycan; 120
KW cartilage compressibility; cartilage elasticity; arthritic disease; 120
KW osteoarthritis; cartilage degradation; inflammatory joint disease; 120
KW aggrecanase-1; ADAMTS-4; aggrecanase-2; ADAMTS-5; thrombospondin domain; 180
KW TSP domain; osteopathic; antiarthritic; cytosolic; antiinflammatory; 180
KW antineumatic; ophthalmological; thrombolytic; vasotropic; antimicrobial; 180
KW respiratory-gen; neutropic; neuroprotective; antiparkinsonian; 240
KW immunosuppressive; aggrecanase inhibition; cancer; rheumatoid arthritis; 240
KW Crohn's disease; corneal ulceration; coronary thrombosis; 240
KW Crohn's disease; emphysema; Alzheimer's disease; Parkinson's disease; 240
KW multiple sclerosis; aortic aneurysm; enzyme; human. 240
XX OS Homo sapiens. 300
XX PN WO2003066822-A2. 300
XX PD 14-AUG-2003. 360
XX PF 05-FEB-2003; 2003WO-US003554. 360
XX PR 05-FEB-2002; 2002US-0354592P. 420
XX PA (AMHP) WYETH. 420
XX PI Georgiadis K, Crawford TK, Tomkinson KN, Morris EA, Racie L; 480
XX DR WPI; 2003-731495/69. 480
XX DR N-PSDB; ADB85504. 480
XX PT New biologically-active aggrecanase protein having a deletion of all, or 540
XX PT a portion of a TSP domain, useful for treating osteoarthritis, cancer, 540
XX PT Parkinson's disease, coronary thrombosis, Alzheimer's disease and 540
XX PT multiple sclerosis. 540
XX PS Disclosure; Fig 11; 11lpp; English. 600
XX CC This invention relates to novel truncated human aggrecanase proteins and 660
XX CC nucleotide sequences. Aggrecan is a major extracellular component of 660
XX CC articular cartilage. It is a proteoglycan responsible for providing 660
XX CC cartilage with its mechanical properties of compressibility and 660
XX CC elasticity. The loss of aggrecan has been implicated in the degradation 660
XX CC of articular cartilage in arthritic diseases such as osteoarthritis. 660
XX CC Aggrecanase is responsible for the cleavage of aggrecan, thereby having a 660
XX CC role in cartilage degradation associated with osteoarthritis and 660
XX CC inflammatory joint disease. The proteins of the current invention are 660
XX CC truncated aggrecanase-1 (ADAMTS-4) and aggrecanase-2 (ADAMTS-5) enzymes 660
XX CC which have at least one thrombospondin (TSP) domain deleted. These are 660
XX CC biologically active and have greater stability and higher expression than 660
XX CC their full-length counterparts. The proteins of the invention may be of 660
XX CC use in the development of compounds with osteopathic, antiarthritic, 660
XX CC cytosolic, antiinflammatory, antineumatic, ophthalmological, 660
XX CC thrombolytic, vasotropic, antimicrobial, respiratory-gen, neutropic, 660
XX CC neuroprotective, antiparkinsonian or immunosuppressive activities through 660
XX CC aggrecanase inhibition. The proteins of the invention may therefore be 660
XX CC useful for the manufacture of compositions for the treatment of 660
XX CC aggrecanase-associated conditions, such as osteoarthritis, cancer, 660
XX CC inflammatory joint disease, rheumatoid arthritis, septic arthritis, 660
XX CC corneal ulceration, coronary thrombosis, Crohn's disease, emphysema, 660
XX CC Alzheimer's disease, Parkinson's disease, multiple sclerosis and aortic 660
XX CC aneurysm. The present sequence is the full-length amino acid sequence of 660
XX CC the aggrecanase-1 (ADAMTS-4) enzyme which was used to create the 660
XX CC truncated aggrecanase-1 proteins of the invention. 660
XX SQ Sequence 837 AA; 660
Query Match 99.9%; Score 4566; DB 7; Length 837; 60
Best Local Similarity 99.9%; Pred. No. 0; 60
Matches 836; Conservative 0; Mismatches 1; Indels 0; Gaps 0; 60
XX 1 MSQTSHPGRGLAGWLGAPQCLLPVPLSWLWLLLLLSLPSARLASPLPREEE 60
DB 1 MSQTSHPGRGLAGWLGAPQCLLPVPLSWLWLLLLLSLPSARLASPLPREEE 60

QY 61 IVFEKLNGSVLPQSGAPARLLCRLOAFGETLLELEQDSGVQVEGLTVQYLGAPELLG 120
DB 61 IVFEKLNGSVLPQSGAPARLLCRLOAFGETLLELEQDSGVQVEGLTVQYLGAPELLG 120
QY 121 GAEPGYTLTGTINGDPESVASLHWGEGGALLGVQVRAELHLQPLEGGTPNSAGPGGAIH 180
DB 121 GAEPGYTLTGTINGDPESVASLHWGEGGALLGVQVRAELHLQPLEGGTPNSAGPGGAIH 180
QY 181 LRRKSPASGQGMCMCNKAPLSPSPRRPRKRAFLSRFVETLVVADDKMAAFHAGLGR 240
DB 181 LRRKSPASGQGMCMCNKAPLSPSPRRPRKRAFLSRFVETLVVADDKMAAFHAGLGR 240
QY 241 YLLTWMAAAAKAFKHPISIRNPVSLVTLVILGSEEGEPQVGPSAAQTLRSCAWORGLN 300
DB 241 YLLTWMAAAAKAFKHPISIRNPVSLVTLVILGSEEGEPQVGPSAAQTLRSCAWORGLN 300
QY 301 TPEDSDPDHFDFTAILFTQDLGCVSTCTGLMADVTVCDPARSCAIYEDDGLQSAFTAA 360
DB 301 TPEDSDPDHFDFTAILFTQDLGCVSTCTGLMADVTVCDPARSCAIYEDDGLQSAFTAA 360
QY 361 HELGHVFNMLHDNSKPCISLNGPLSTSRHVMAVMAHVDPEPWPSPCSARFITDLDNGY 420
DB 361 HELGHVFNMLHDNSKPCISLNGPLSTSRHVMAVMAHVDPEPWPSPCSARFITDLDNGY 420
QY 421 GHCLLDKPEAPLHLVPTFPFGKDYDADRCQLTFFGDSRHCPQLPPCAALMCSGHLNGHA 480
DB 421 GHCLLDKPEAPLHLVPTFPFGKDYDADRCQLTFFGDSRHCPQLPPCAALMCSGHLNGHA 480
QY 481 MCQTKHSPWADGTPCGPAQACMGGRCLHMDQLQDNIPQAGGWPWGDCSRTCCGGV 540
DB 481 MCQTKHSPWADGTPCGPAQACMGGRCLHMDQLQDNIPQAGGWPWGDCSRTCCGGV 540
QY 541 QFSSRDCTPVPNRNGSKYCEGRTRFRSCNTDCTGSGALTFRQCAAYNHTDLFKSF 600
DB 541 QFSSRDCTPVPNRNGSKYCEGRTRFRSCNTDCTGSGALTFRQCAAYNHTDLFKSF 600
QY 601 PGPMWVPRYTVGAPQDQCKLFCQARALGYVYVLPBPRVVDGTPCSPDSSVCQRCIHA 660
DB 601 PGPMWVPRYTVGAPQDQCKLFCQARALGYVYVLPBPRVVDGTPCSPDSSVCQRCIHA 660
QY 661 GCDRIIGSKKPKDKCMVCGGSGGSKGSKGSKGSKGSKGSKGSKGSKGSKGSKGSKG 720
DB 661 GCDRIIGSKKPKDKCMVCGGSGGSKGSKGSKGSKGSKGSKGSKGSKGSKGSKGSKG 720
QY 721 GHRSIYALKLKPDGVALNGEYTLMPSPDTPVLPVAVSLRYSGLATASSETLSGHGPLAOP 780
DB 721 GHRSIYALKLKPDGVALNGEYTLMPSPDTPVLPVAVSLRYSGLATASSETLSGHGPLAOP 780
QY 781 LTLQVLVAGNPQDTRLYRFFVPRTPPTPPTPQDHLHRAQILILRRRPMWAGRK 837
DB 781 LTLQVLVAGNPQDTRLYRFFVPRTPPTPPTPPTPQDHLHRAQILILRRRPMWAGRK 837
RESULT 7
AAB21256
ID AAB21256 standard; protein; 840 AA.
XX AAB21256;
AC AAB21256;
XX 23-FEB-2001 (first entry)
DE Human metalloproteinase KIAA0688.
XX Human; KIAA0688; metalloproteinase; ADAM;
KW a disintegrin and metalloproteinase domain; thrombospondin domain;
KW vaccine; neutropic; neuroprotective; antiparkinsonian; cerebrotective;
KW cytosolic; antiarthritic; immunosuppressive; Alzheimer's disease;
KW Parkinson's disease; stroke; cancer; arthritis; autoimmune disease;
KW brain tumour; brain injury.
XX Homo sapiens.
OS
XX

PR	17-SEP-1998;	98US-010684P.
PR	17-SEP-1998;	98US-0100710P.
PR	17-SEP-1998;	98US-0100711P.
PR	17-SEP-1998;	98US-0100919P.
PR	17-SEP-1998;	98US-0100930P.
PR	18-SEP-1998;	98US-0100848P.
PR	18-SEP-1998;	98US-0100849P.
PR	18-SEP-1998;	98US-0101014P.
PR	18-SEP-1998;	98US-0101068P.
PR	18-SEP-1998;	98US-0101071P.
PR	22-SEP-1998;	98US-0101279P.
PR	23-SEP-1998;	98US-0101471P.
PR	23-SEP-1998;	98US-0101472P.
PR	23-SEP-1998;	98US-0101474P.
PR	23-SEP-1998;	98US-0101475P.
PR	23-SEP-1998;	98US-0101476P.
PR	23-SEP-1998;	98US-0101477P.
PR	24-SEP-1998;	98US-0101738P.
PR	24-SEP-1998;	98US-0101741P.
PR	24-SEP-1998;	98US-0101743P.
PR	24-SEP-1998;	98US-0101915P.
PR	24-SEP-1998;	98US-0101916P.
PR	29-SEP-1998;	98US-0102207P.
PR	29-SEP-1998;	98US-0102240P.
PR	29-SEP-1998;	98US-0102307P.
PR	29-SEP-1998;	98US-0102330P.
PR	29-SEP-1998;	98US-0102331P.
PR	30-SEP-1998;	98US-0102484P.
PR	30-SEP-1998;	98US-0102487P.
PR	30-SEP-1998;	98US-0102570P.
PR	30-SEP-1998;	98US-0102571P.
PR	01-OCT-1998;	98US-0102684P.
PR	01-OCT-1998;	98US-0102687P.
PR	02-OCT-1998;	98US-0102965P.
PR	06-OCT-1998;	98US-0103258P.
PR	06-OCT-1998;	98US-0103449P.
PR	07-OCT-1998;	98US-0103314P.
PR	07-OCT-1998;	98US-0103315P.
PR	07-OCT-1998;	98US-0103328P.
PR	07-OCT-1998;	98US-0103395P.
PR	07-OCT-1998;	98US-0103396P.
PR	07-OCT-1998;	98US-0103401P.
PR	08-OCT-1998;	98US-0103633P.
PR	08-OCT-1998;	98US-0103678P.
PR	08-OCT-1998;	98US-0103679P.
PR	14-OCT-1998;	98US-0103711P.
PR	20-OCT-1998;	98US-0104257P.
PR	20-OCT-1998;	98US-0104967P.
PR	20-OCT-1998;	98US-0105000P.
PR	21-OCT-1998;	98US-0105002P.
PR	21-OCT-1998;	98US-0105104P.
PR	22-OCT-1998;	98US-0105169P.
PR	22-OCT-1998;	98US-0105266P.
PR	26-OCT-1998;	98US-0105693P.
PR	26-OCT-1998;	98US-0105694P.
PR	27-OCT-1998;	98US-0105807P.
PR	27-OCT-1998;	98US-0105881P.
PR	27-OCT-1998;	98US-0105882P.
PR	27-OCT-1998;	98US-0106062P.
PR	28-OCT-1998;	98US-0106023P.
PR	28-OCT-1998;	98US-0106029P.
PR	28-OCT-1998;	98US-0106030P.
PR	28-OCT-1998;	98US-0106032P.
PR	28-OCT-1998;	98US-0106033P.
PR	28-OCT-1998;	98US-0106178P.
PR	29-OCT-1998;	98US-0106248P.
PR	29-OCT-1998;	98US-0106384P.
PR	29-OCT-1998;	98US-0108500P.
PR	03-NOV-1998;	98US-0106484P.
PR	03-NOV-1998;	98US-0106856P.
PR	03-NOV-1998;	98US-0106902P.
PR	03-NOV-1998;	98US-0106905P.

XX	03-NOV-1998;	98US-0106919P.
PR	03-NOV-1998;	98US-0106932P.
PR	03-NOV-1998;	98US-0106934P.
PR	10-NOV-1998;	98US-0107783P.
PR	17-NOV-1998;	98US-0108775P.
PR	17-NOV-1998;	98US-0108779P.
PR	17-NOV-1998;	98US-0108787P.
PR	17-NOV-1998;	98US-0108788P.
PR	17-NOV-1998;	98US-0108801P.
PR	17-NOV-1998;	98US-0108802P.
PR	17-NOV-1998;	98US-0108806P.
PR	17-NOV-1998;	98US-0108807P.
PR	17-NOV-1998;	98US-0108867P.
PR	18-NOV-1998;	98US-0108867P.
PR	18-NOV-1998;	98US-0108848P.
PR	18-NOV-1998;	98US-0108849P.
PR	18-NOV-1998;	98US-0108850P.
PR	18-NOV-1998;	98US-0108851P.
PR	18-NOV-1998;	98US-0108852P.
PR	18-NOV-1998;	98US-0108858P.
PR	18-NOV-1998;	98US-0108904P.
XX	(GETH) GENENTECH INC.	
PA	Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;	
PI	WPI; 2000-237871/20.	
XX	N-PSDB; AAA37111.	
DR	New mammalian DNA sequences encoding transmembrane, receptor or secreted	
XX	PRO polypeptides, useful for screening of potential peptide or small	
PT	molecule inhibitors of the relevant receptor/ligand interactions.	
PT	Claim 12; Fig 180	

Db 301 TPEDSGPDHFDTAILFTRODLGCVSTCDTLGADVGTVCDPARSCAIVDDGLQSAFTAA 360
 QY 361 HELGHVFNMLHNSKPCISLNGPLSTSRHVMAVPMVAHVDPPEPWPSCSARFITTDFLDNGY 420
 Db 361 HELGHVFNMLHNSKPCISLNGPLSTSRHVMAVPMVAHVDPPEPWPSCSARFITTDFLDNGY 420
 QY 421 GHCLLDKPEAPLHLVPTFGKDYADROCOLTFTGPDSDRHCPLPPPCAALWCSGHLNGHA 480
 Db 421 GHCLLDKPEAPLHLVPTFGKDYADROCOLTFTGPDSDRHCPLPPPCAALWCSGHLNGHA 480
 QY 481 MCQTKHSPWADGTPCGPAQACMGRCCLHMDQLQDFNIPOAGGWPWPGDSCRTCCGGV 540
 Db 481 MCQTKHSPWADGTPCGPAQACMGRCCLHMDQLQDFNIPOAGGWPWPGDSCRTCCGGV 540
 QY 541 QFSRDCTRPVPRNGKCYCEGRTRFRSCNTEDCPTGSALTFRFEOCAAYNHRITDLFKSF 600
 Db 541 QFSRDCTRPVPRNGKCYCEGRTRFRSCNTEDCPTGSALTFRFEOCAAYNHRITDLFKSF 600
 QY 601 PGPMWVPRYTGVAPODQCKLTQARALGYVYVLEPRVVDGTPCSPDSSSVCVQGRCIHA 660
 Db 601 PGPMWVPRYTGVAPODQCKLTQARALGYVYVLEPRVVDGTPCSPDSSSVCVQGRCIHA 660
 QY 661 GCDRIIGSKKFKDKCMVCGDGGSGCSKQSGSFRKFRYGYNNVVTIPAGATHILVRQOQNP 720
 Db 661 GCDRIIGSKKFKDKCMVCGDGGSGCSKQSGSFRKFRYGYNNVVTIPAGATHILVRQOQNP 720
 QY 721 GHRISYIALKLPDGSYALNGEYTLMPSPDVLPGAVSLRYSGATAAETLSGHGFLAQP 780
 Db 721 GHRISYIALKLPDGSYALNGEYTLMPSPDVLPGAVSLRYSGATAAETLSGHGFLAQP 780
 QY 781 LTLQVLVAGNQDTRLRYFFVPRPTPTPTQDMLHRRQAQILBILRRRFPWAGRK 837
 Db 781 LTLQVLVAGNQDTRLRYFFVPRPTPTPTQDMLHRRQAQILBILRRRFPWAGRK 837

RESULT 9
 AAB66178
 ID AAB66178 standard; protein; 837 AA.
 XX
 AC AAB66178;
 XX
 DT 02-APR-2001 (first entry)
 XX
 DE Protein of the invention #90.
 XX
 KW Secreted; transmembrane; gene therapy.
 XX
 OS Unidentified.
 XX
 PN WO2000/78961-A1.
 XX
 PD 28-DEC-2000.
 XX
 PF 18-FEB-2000; 2000WO-US004342.
 XX
 PR 23-JUN-1999; 99US-0141037P.
 PR 20-JUL-1999; 99US-0144758P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 01-SEP-1999; 99WO-US020111.
 PR 29-OCT-1999; 99US-01632506P.
 PR 30-NOV-1999; 99WO-US028313.
 PR 02-DEC-1999; 99WO-US028551.
 PR 16-DEC-1999; 99WO-US030095.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000376.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
 PI Cao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
 PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
 PI Williams PM, Wood WI;

DR WPI; 2001-071395/08.
 XX Secreted and transmembrane proteins and nucleic acids designated PRO,
 PT useful as hybridization probes, in chromosome and gene mapping and gene
 PT therapy.
 XX Claim 1; Fig 180; 787pp; English.
 XX The present invention relates to secreted and transmembrane proteins.
 CC These proteins and the DNA encoding them may be used as hybridization
 CC probes, in chromosome and gene mapping and in the generation of anti-
 CC sense RNA and DNA. They may also be used to generate either
 CC transgenic animals or knockout animals which are in turn useful for
 CC development and screening of therapeutically useful reagents. The nucleic
 CC acids may also be used in gene therapy
 XX Sequence 837 AA;
 SQ

Query Match 99.8%; Score 4563; DB 4; Length 837;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 836; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSQTGSHFPGRLAGRWLWGAQPCILLPIVPLSWLWLLLLILLASLLPSARLASPLPREE 60
 Db 1 MSQTGSHFPGRLAGRWLWGAQPCILLPIVPLSWLWLLLLILLASLLPSARLASPLPREE 60
 QY 61 IVFPEKLNGSVLPGSGAPARLLCRLOAFGETLLELEODSGVQVEGLTVQYLQOAPPELLG 120
 Db 61 IVFPEKLNGSVLPGSGAPARLLCRLOAFGETLLELEODSGVQVEGLTVQYLQOAPPELLG 120
 QY 121 GAEPGTLYLTGTINGDPESVASLHWDGGALLGVLYRGAEHLQPLEGGTTPNSAGGFGAHI 180
 Db 121 GAEPGTLYLTGTINGDPESVASLHWDGGALLGVLYRGAEHLQPLEGGTTPNSAGGFGAHI 180
 QY 181 LRRKSPASQGGPWCNVKAPLGSPSPRRPRAKFASLSRFVETLVVADDDKMAAFHAGLAKR 240
 Db 181 LRRKSPASQGGPWCNVKAPLGSPSPRRPRAKFASLSRFVETLVVADDDKMAAFHAGLAKR 240
 QY 241 YLLTVMAAAAKAFKPSIRNPVSLVTVLILGSGEEGPQVGPSSAAQTLSFCAMORGLN 300
 Db 241 YLLTVMAAAAKAFKPSIRNPVSLVTVLILGSGEEGPQVGPSSAAQTLSFCAMORGLN 300
 QY 301 TPEDSDPDHFDTAILFTRODLGCVSTCDTLGADVGTVCDPARSCAIVDDGLQSAFTAA 360
 Db 301 TPEDSDPDHFDTAILFTRODLGCVSTCDTLGADVGTVCDPARSCAIVDDGLQSAFTAA 360
 QY 361 HELGHVFNMLHNSKPCISLNGPLSTSRHVMAVPMVAHVDPPEPWPSCSARFITTDFLDNGY 420
 Db 361 HELGHVFNMLHNSKPCISLNGPLSTSRHVMAVPMVAHVDPPEPWPSCSARFITTDFLDNGY 420
 QY 421 GHCLLDKPEAPLHLVPTFGKDYADROCOLTFTGPDSDRHCPLPPPCAALWCSGHLNGHA 480
 Db 421 GHCLLDKPEAPLHLVPTFGKDYADROCOLTFTGPDSDRHCPLPPPCAALWCSGHLNGHA 480
 QY 481 MCQTKHSPWADGTPCGPAQACMGRCCLHMDQLQDFNIPOAGGWPWPGDSCRTCCGGV 540
 Db 481 MCQTKHSPWADGTPCGPAQACMGRCCLHMDQLQDFNIPOAGGWPWPGDSCRTCCGGV 540
 QY 541 QFSRDCTRPVPRNGKCYCEGRTRFRSCNTEDCPTGSALTFRFEOCAAYNHRITDLFKSF 600
 Db 541 QFSRDCTRPVPRNGKCYCEGRTRFRSCNTEDCPTGSALTFRFEOCAAYNHRITDLFKSF 600
 QY 601 PGPMWVPRYTGVAPODQCKLTQARALGYVYVLEPRVVDGTPCSPDSSSVCVQGRCIHA 660
 Db 601 PGPMWVPRYTGVAPODQCKLTQARALGYVYVLEPRVVDGTPCSPDSSSVCVQGRCIHA 660
 QY 661 GCDRIIGSKKFKDKCMVCGDGGSGCSKQSGSFRKFRYGYNNVVTIPAGATHILVRQOQNP 720
 Db 661 GCDRIIGSKKFKDKCMVCGDGGSGCSKQSGSFRKFRYGYNNVVTIPAGATHILVRQOQNP 720
 QY 721 GHRISYIALKLPDGSYALNGEYTLMPSPDVLPGAVSLRYSGATAAETLSGHGFLAQP 780
 Db 721 GHRISYIALKLPDGSYALNGEYTLMPSPDVLPGAVSLRYSGATAAETLSGHGFLAQP 780

QY 781 LTLQVLVAGNPQTRLYSFFVPRPTPTPQDMLHRRRAQILILRRRPWAGRK 837
DB 781 LTLQVLVAGNPQTRLYSFFVPRPTPTPQDMLHRRRAQILILRRRPWAGRK 837

RESULT 10
AAU29199
ID AAU29199 standard; protein; 837 AA.
XX AAU29199;
XX 18-DEC-2001 (first entry)
XX Human PRO polypeptide sequence #176.
XX PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
XX Homo sapiens.
XX WC200168848-A2.
XX 20-SEP-2001.
XX 28-FEB-2001; 2001WO-US006520.
XX 01-MAR-2000; 2000WO-US005601.
XX 02-MAR-2000; 2000WO-US005841.
XX 03-MAR-2000; 2000US-0187202P.
XX 06-MAR-2000; 2000US-0186968P.
XX 14-MAR-2000; 2000US-0189320P.
XX 14-MAR-2000; 2000US-0189328P.
XX 15-MAR-2000; 2000WO-US006884.
XX 21-MAR-2000; 2000US-0190828P.
XX 21-MAR-2000; 2000US-0191007P.
XX 21-MAR-2000; 2000US-0191048P.
XX 21-MAR-2000; 2000US-0191314P.
XX 28-MAR-2000; 2000US-0192655P.
XX 29-MAR-2000; 2000US-0193032P.
XX 30-MAR-2000; 2000US-0193053P.
XX 30-MAR-2000; 2000WO-US008439.
XX 04-APR-2000; 2000US-0194449P.
XX 04-APR-2000; 2000US-0194647P.
XX 11-APR-2000; 2000US-0195975P.
XX 11-APR-2000; 2000US-0196000P.
XX 11-APR-2000; 2000US-0196187P.
XX 11-APR-2000; 2000US-0196690P.
XX 11-APR-2000; 2000US-0196820P.
XX 18-APR-2000; 2000US-0198121P.
XX 18-APR-2000; 2000US-0198585P.
XX 25-APR-2000; 2000US-0199397P.
XX 25-APR-2000; 2000US-0199550P.
XX 25-APR-2000; 2000US-0199654P.
XX 03-MAY-2000; 2000US-0201516P.
XX 22-MAY-2000; 2000WO-US013705.
XX 22-MAY-2000; 2000WO-US014042.
XX 30-MAY-2000; 2000WO-US014941.
XX 02-JUN-2000; 2000WO-US015264.
XX 05-JUN-2000; 2000US-0209832P.
XX 28-JUL-2000; 2000WO-US020710.
XX 22-AUG-2000; 2000US-0064848.
XX 24-AUG-2000; 2000WO-US023328.
XX 08-NOV-2000; 2000WO-US030952.
XX 01-DEC-2000; 2000WO-US032678.
XX 20-DEC-2000; 2000WO-US034956.
XX (GETH) GENENTECH INC.
XX Baker KP, Chen J, Deanyoyers L, Goddard A, Godowski PJ, Gurney AL;
XX Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;

XX WPI: 2001-602746/68.
DR N-PSDB; AAS46100.
XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the
PT presence of tumors, such as prostate and breast tumors, in mammals and to
PT screen for modulators of the compounds.
XX Claim 11; Fig 352; 774pp; English.
XX Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
CC The PRO polypeptides and their associated nucleic acids can be used to
CC detect the presence of a tumour in a mammal by comparing the level of
CC expression of a PRO polypeptide in a test sample of cells from the animal
CC and a control sample of normal cells, whereby a higher level of
CC expression in the test sample indicates the presence of a tumour in the
CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
CC and rabbits but are preferably human. The polypeptides can be used to
CC stimulate tumour necrosis factor (TNF) alpha release from human blood,
CC when contacted with it. A specific polypeptide can be used to stimulate
CC the proliferation or differentiation of chondrocyte cells. The PRO
CC proteins can be used to determine the presence of tumours and also
CC susceptibility to tumour development, particularly adrenal, lung, colon,
CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC can be used for genetic analysis of individuals with genetic disorders
XX Sequence 837 AA;
SQ

Query Match 99.8%; Score 4563; DB 4; Length 837;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 836; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSQTGSHPCGRGLACRWLWGAQPCILLPIVPLSWLWLLLLASLLPSARLASPLPREE 60
DB 1 MSQTGSHPCGRGLACRWLWGAQPCILLPIVPLSWLWLLLLASLLPSARLASPLPREE 60
QY 61 IVFPEKLSVLPVPGSGAPARLLCRLOAFGCTLLLEQDSGVQVEGLTVQYLGAPELLG 120
DB 61 IVFPEKLSVLPVPGSGAPARLLCRLOAFGCTLLLEQDSGVQVEGLTVQYLGAPELLG 120
QY 121 GAEPGYLTGTINGDPDESVAHLWDGALLGVLYRGAEHLHLOPLEGGTNSAGGGAHI 180
DB 121 GAEPGYLTGTINGDPDESVAHLWDGALLGVLYRGAEHLHLOPLEGGTNSAGGGAHI 180
QY 181 LRKSPASGCGMNCNVKAPLGSPSPRRPRAKPASPILSRFVETLVVADDDKMAAFHGLKX 240
DB 181 LRKSPASGCGMNCNVKAPLGSPSPRRPRAKPASPILSRFVETLVVADDDKMAAFHGLKX 240
QY 241 YLLTVMAAAKAFKHPISIRNPVSLVTVRLVILSGEGEPQVGPSSAQTLSFCAWQGLN 300
DB 241 YLLTVMAAAKAFKHPISIRNPVSLVTVRLVILSGEGEPQVGPSSAQTLSFCAWQGLN 300
QY 301 TPEDSDPDHFDTAILFTRODLGVSTCDTLGMADVTCVCDPARSCAIVEDDGLQSAFTAA 360
DB 301 TPEDSDPDHFDTAILFTRODLGVSTCDTLGMADVTCVCDPARSCAIVEDDGLQSAFTAA 360
QY 361 HELGHVFNMLHNSKPCISLNGPLSTRHVMAVMAHVPDPEEPWSCSARFIFDLDNGY 420
DB 361 HELGHVFNMLHNSKPCISLNGPLSTRHVMAVMAHVPDPEEPWSCSARFIFDLDNGY 420
QY 421 GHCLLDKPEAPLHLPVTFPGKYDADRCQLTFGPDSTRHCQPLPPPPCAALWCSGHLNGHA 480
DB 421 GHCLLDKPEAPLHLPVTFPGKYDADRCQLTFGPDSTRHCQPLPPPPCAALWCSGHLNGHA 480
QY 481 MCOTKSPWADGTPCGPAQCMGRCCLHMDOLDFNIPOAGGKGPWGPCDCCSRTCCGGV 540
DB 481 MCOTKSPWADGTPCGPAQCMGRCCLHMDOLDFNIPOAGGKGPWGPCDCCSRTCCGGV 540
QY 541 QFSRDCTRPVPRNGKYCEGRTRFRSCNTECDPTGSGALTFFREEQCAAYNHRITDLFKSF 600
DB 541 QFSRDCTRPVPRNGKYCEGRTRFRSCNTECDPTGSGALTFFREEQCAAYNHRITDLFKSF 600

QY 601 PGMWVPRYTGVAPOQCKLTQCARALGYVYVLEPRVVDGTPCSPDSSVCVQGRCIHA 660
DB 601 PGMWVPRYTGVAPOQCKLTQCARALGYVYVLEPRVVDGTPCSPDSSVCVQGRCIHA 660
QY 661 GCDRIIGSKKPKDKWVCGDGGCKSQSGSKFPRFYGVNNVTIPAGATHILVROQGNP 720
DB 661 GCDRIIGSKKPKDKWVCGDGGCKSQSGSKFPRFYGVNNVTIPAGATHILVROQGNP 720
QY 721 GHRSIYLALKLPDGSYALNGEYTLMPSTDDVLPGLVSLRYSGATAASETLSGHGFLAOP 780
DB 721 GHRSIYLALKLPDGSYALNGEYTLMPSTDDVLPGLVSLRYSGATAASETLSGHGFLAOP 780
QY 781 LTLQVLVAGNPQDRLRYSFVPRPTSPRPPQDMLHRRQAQILRLRRPWAGRK 837
DB 781 LTLQVLVAGNPQDRLRYSFVPRPTSPRPPQDMLHRRQAQILRLRRPWAGRK 837

RESULT 11
ABU58575
ID ABU58575 standard; protein; 837 AA.
AC ABU58575;
XX
DT 15-APR-2003 (first entry)
XX
DE Human PRO polypeptide #176.
XX
KW Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;
KW dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT;
KW antibody-dependent enzyme mediated prodrug therapy.
XX
OS Homo sapiens.
XX
PN
XX
PD US2003027272-A1.
XX
PF 06-FEB-2003.
XX
PP 21-JUN-2002; 2002US-00176492.
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 17-OCT-1997; 97US-0062250P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 28-OCT-1997; 97US-0063540P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063564P.
PR 31-OCT-1997; 97US-0063734P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066120P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066772P.
PR 11-DEC-1997; 97US-0069335P.
PR 12-DEC-1997; 97US-0069425P.
PR 17-DEC-1997; 97US-0069870P.
PR 18-DEC-1997; 97US-0068017P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
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PR 31-MAR-1998; 98US-0080194P.
PR 01-APR-1998; 98US-0080327P.
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PR 02-JUN-1998; 98US-0087609P.
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PR 16-JUN-1998; 98US-0089105P.
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PR 25-JUN-1998; 98US-0090690P.
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PR 25-JUN-1998; 98US-0090696P.

KW tumour necrosis factor-alpha release; TNF-alpha release;
KW chondrocyte proliferation; chondrocyte differentiation; tumour;
KW adrenal tumour; lung tumour; colon tumour; breast tumour;
KW prostate tumour; rectal tumour; cervical tumour; liver tumour.

XX OS Homo sapiens.

XX PN US2003032127-A1.

XX XX 13-FEB-2003.

XX PP 26-JUN-2002; 2002US-00183012.

XX XX 18-SEP-1997; 97US-0059263P.

PR 18-SEP-1997; 97US-0059266P.

PR 17-OCT-1997; 97US-0062250P.

PR 21-OCT-1997; 97US-0063486P.

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PR 11-DEC-1997; 97US-00693335P.
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PR 17-DEC-1997; 97US-00698707P.
PR 18-DEC-1997; 97US-00690171P.
PR 10-MAR-1998; 98US-00774507P.
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PR 11-MAR-1998; 98US-00778866P.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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5	2135	46.7	967	4	US-09-130-491-2
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24	1086	23.8	481	4	US-09-130-491-8
25	1059	23.2	518	3	US-09-369-364A-22
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39	639	14.0	245	3	US-09-369-364A-11	Sequence 10, Appl
40	547.5	12.0	507	4	US-09-963-791-10	Sequence 20, Appl
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ALIGNMENTS

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; Sequence 2, Application US/09122126B
; Patent No. 6451575
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: AGGREGAN DEGRADING METALLO PROTEASES
; FILE REFERENCE: DM6909
; CURRENT APPLICATION NUMBER: US/09/122,126B
; CURRENT FILING DATE: 1998-07-24
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 837
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-122-126B-2

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RESULT 2
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; Sequence 2, Application US/09634286A
; Patent No. 6521436
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: AGGREGAN DEGRADING METALLO PROTEASES
; FILE REFERENCE: DM6909A
; CURRENT APPLICATION NUMBER: US/09/634, 286A
; CURRENT FILING DATE: 2000-08-09
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 837
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-634-286A-2

	Query Match	100.0%;	Score 4570;	DB 4;	Length 837;	
	Best Local Similarity	100.0%;	Prod. No. 0;			
	Matches 837;	Conservative	0;	Mismatches	0;	Indels
						Gaps 0;
QY	1	MSQTGSHPRGRLAGRWLNGAOPCLLLPTVPISWLWVLLLLLLASLLPSARLASPLPREE	60			
Db	1	MSQTGSHPRGRLAGRWLNGAOPCLLLPTVPISWLWVLLLLLLASLLPSARLASPLPREE	60			
QY	61	IVFPEKLSVLPGSGAPARLLCRLOAQGETLLLELEQDSGVQVEGLTVQVIGQAPELLG	120			
Db	61	IVFPEKLSVLPGSGAPARLLCRLOAQGETLLLELEQDSGVQVEGLTVQVIGQAPELLG	120			
QY	121	GAEPCTYLTGTINGDPESVASIHWDDGALLGVLYRGAEHLHLPLEGGTPNSAGGPGGAAH	180			
Db	121	GAEPCTYLTGTINGDPESVASIHWDDGALLGVLYRGAEHLHLPLEGGTPNSAGGPGGAAH	180			
QY	181	LRRKSPASGGQPMCNVKAFLGSPSPRRRAKRFASLSRFVETLVVADDDKMAAFHGAGLKR	240			
Db	181	LRRKSPASGGQPMCNVKAFLGSPSPRRRAKRFASLSRFVETLVVADDDKMAAFHGAGLKR	240			
QY	241	YLLTTWAAAATAAKFKHPSIRNPVSLVYVTRLVILGSGEEGPOVCPSPAQTLRSPCAWQRGIN	300			
Db	241	YLLTTWAAAATAAKFKHPSIRNPVSLVYVTRLVILGSGEEGPOVCPSPAQTLRSPCAWQRGIN	300			
QY	301	TPEDSDPHDFTAILLFTRQDLGCVSTCDTGLGMADVTGCDPARS CAIIVDDGLOSAFTAA	360			

301	TPEDSDPHFDTAAILFTRQDL	CGVSTCDTLGMADVGTCDPARSCAI	VEDDGLQSAFTAA	360		
361	HELGHVFNNMLHDNSKPCISL	NGPISTSRHWYAPMAHVPDEEP	WSPSCSARFITDFLDNGY	420		
361	HELGHVFNNMLHDNSKPCISL	NGPISTSRHWYAPMAHVPDEEP	WSPSCSARFITDFLDNGY	420		
421	GHCLLDKPEAPLHLVPVTF	PGKYDADRCQCLTFGPDSRHCP	QLPPPCAALWCSGHLNGHA	480		
421	GHCLLDKPEAPLHLVPVTF	PGKYDADRCQCLTFGPDSRHCP	QLPPPCAALWCSGHLNGHA	480		
481	MCQTKHSPWADGTPCGPAQA	CMWGRCLHMDQLQDLFNI	POAGGMPGMPGWD	CSRTC	CGGVY	540
481	MCQTKHSPWADGTPCGPAQA	CMWGRCLHMDQLQDLFNI	POAGGMPGMPGWD	CSRTC	CGGVY	540
541	QFSRSDCTRPVRNGGKYCE	GRRTFRSCNTECPTGSALT	FRFEEQCAA	NHRTDL	PKF	600
541	QFSRSDCTRPVRNGGKYCE	GRRTFRSCNTECPTGSALT	FRFEEQCAA	NHRTDL	PKF	600
601	PGPMDWVRYTGVAPQDOCKL	TCQARALGYYYVLEPRVVDG	TFPCSPDSSVCVQGR	CIHA	660	
601	PGPMDWVRYTGVAPQDOCKL	TCQARALGYYYVLEPRVVDG	TFPCSPDSSVCVQGR	CIHA	660	
661	GCDRIIGSKKPKDKMWCG	SGSGSKQSGSFRKFRYGNNV	VTIPAGATHILVROQGNP	720		
661	GCDRIIGSKKPKDKMWCG	SGSGSKQSGSFRKFRYGNNV	VTIPAGATHILVROQGNP	720		
721	GHRSYLAUKLPDGSYALNGE	YTLMPSPDVLVLPAGVSLRY	SAGATASETLSHG	HG	PLAQ	780
721	GHRSYLAUKLPDGSYALNGE	YTLMPSPDVLVLPAGVSLRY	SAGATASETLSHG	HG	PLAQ	780
781	LTLQVLVAGNPQDTRLRY	SFFVPRTPTSTPRPTQD	MLHRRAQILLEILRR	RRP	WAGRK	837
781	LTLQVLVAGNPQDTRLRY	SFFVPRTPTSTPRPTQD	MLHRRAQILLEILRR	RRP	WAGRK	837

RESULT 3

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RESUM. 3
US-10-247-685-2
; Sequence 2, Application US/10247685
; Patent No. 6753176
;
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: AGGREGAN DEGRADING METALLO PROTEASES
; FILE REFERENCE: DM6909D
; CURRENT APPLICATION NUMBER: US/10/247,685
; CURRENT FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 837
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-247-685-2

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	Query Match	100.0%;	Score 4570;	DB 4;	Length 837;
	Best Local Similarity	100.0%;	Prod. No. 0;		
	Matches 837;	Conservative	Mismatches 0;	Indels 0;	Gaps 0
QY	1	MSQTGSHPGRLGRLWLGWGPCLLLPVPSLWLVLLLLLSLLPSARLASPLPREEE	60		
DB	1	MSQTGSHPGRLGRLWLGWGPCLLLPVPSLWLVLLLLLSLLPSARLASPLPREEE	60		
QY	61	IVFPEKLSVLPQSGAPARLLCRLOAFGETLLELEQDSGVVOEGLTVQVIGQAPELLG	120		
DB	61	IVFPEKLSVLPQSGAPARLLCRLOAFGETLLELEQDSGVVOEGLTVQVIGQAPELLG	120		
QY	121	GAEPCTYLTGTINGDPESVASLHWGCGALLGVQYRGAEHLHPLEGGTTPNSAGGPGGAAHI	180		
DB	121	GAEPCTYLTGTINGDPESVASLHWGCGALLGVQYRGAEHLHPLEGGTTPNSAGGPGGAAHI	180		
QY	181	LRRKSPASGGQPMCNVKAPLGSPSPRRPRKRFPASLSRFVETLVVADDKMAFHHAGLKR	240		
DB	181	LRRKSPASGGQPMCNVKAPLGSPSPRRPRKRFPASLSRFVETLVVADDKMAFHHAGLKR	240		


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QY 241 YLTVMAAAKAFKPSIRNPVSLVTRVLVILSGEGPQVPSAAQTLSFCAWQGLN 300
DB 241 YLTVMAAAKAFKPSIRNPVSLVTRVLVILSGEGPQVPSAAQTLSFCAWQGLN 300
QY 301 TPEDSDPDHFDTAILFTRODLGCVSTCDTLGMDVGTVCDPARSCAIVEDDGLQSAFTAA 360
DB 301 TPEDSDPDHFDTAILFTRODLGCVSTCDTLGMDVGTVCDPARSCAIVEDDGLQSAFTAA 360
QY 361 HELGHVFNMLHDSKPCISLNGPLSTRHVMAPVMAHVDPEEPWSPCSARFIITDFLDNGY 420
DB 361 HELGHVFNMLHDSKPCISLNGPLSTRHVMAPVMAHVDPEEPWSPCSARFIITDFLDNGY 420
QY 421 GHCLLDKPEAPLHLPVTFPGKYDADRQCLTFCGDSRHCPCQLPPPCAALWCSGHLNGHA 480
DB 421 GHCLLDKPEAPLHLPVTFPGKYDADRQCLTFCGDSRHCPCQLPPPCAALWCSGHLNGHA 480
QY 481 MCOTKHSPPWADGTPCGPAQACMGRCCLHMDLODFNIPOAGGNGPWPWGDCSRTCGGV 540
DB 481 MCOTKHSPPWADGTPCGPAQACMGRCCLHMDLODFNIPOAGGNGPWPWGDCSRTCGGV 540
QY 541 QFSRDCTRPVPRNGKYCEGRTRFRSCNTEDCPTGSALTFRBEOCAAYNHRTDLFKSF 600
DB 541 QFSRDCTRPVPRNGKYCEGRTRFRSCNTEDCPTGSALTFRBEOCAAYNHRTDLFKSF 600
QY 601 PGPMWVRYTGVAPODQCKLTQCARALGYVYVLEPRVVDGTPCSPDSSVCVQGRCIHA 660
DB 601 PGPMWVRYTGVAPODQCKLTQCARALGYVYVLEPRVVDGTPCSPDSSVCVQGRCIHA 660
QY 661 GCDRIIGSKKFKDKMVCVCGDGGSCSKSGSPKFRFYGYNNVTIIPAGATHILVROQGNP 720
DB 661 GCDRIIGSKKFKDKMVCVCGDGGSCSKSGSPKFRFYGYNNVTIIPAGATHILVROQGNP 720
QY 721 GHRISYIALKLPDGSVALNGEYTLMPSTDVLPGLVSLRYSGATASSETLSHGGLAOP 780
DB 721 GHRISYIALKLPDGSVALNGEYTLMPSTDVLPGLVSLRYSGATASSETLSHGGLAOP 780
QY 781 LTLQVLVAGNPQDTRLRYSFVFPRTPTSTPRTPQDMLHRAQILBILRRRPWAGR 837
DB 781 LTLQVLVAGNPQDTRLRYSFVFPRTPTSTPRTPQDMLHRAQILBILRRRPWAGR 837

RESULT 4
US-09-321-987B-4
; Sequence 4, Application US/09321987B
; Patent No. 6730820
; GENERAL INFORMATION:
; APPLICANT: Kimble, Judith E
; APPLICANT: Bielloch, Robert H
; TITLE OF INVENTION: Agent and Method for Modulating Cell Migration
; FILE REFERENCE: 960296.95386
; CURRENT APPLICATION NUMBER: US/09/321,987B
; CURRENT FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,170
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 60/129,023
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 950
; TYPE: PRT
; ORGANISM: Murine
US-09-321-987B-4

Query Match 47.2%; Score 2158; DB 4; Length 950;
Best Local Similarity 49.4%; Pred. No. 2.9e-154;
Matches 414; Conservative 135; Mismatches 221; Indels 68; Gaps 16;

QY 37 LLLLLL--LLSARIA--SPLPREEEIVFPEKINGSLVPGSGAPARLLCRILQAFGETL 92
DB 18 MLLLLLITMLLCAGAHGRPTEDEELVPSLERA---PGHDSITTRL-RLDAFGQOL 73
QY 93 LLELEQDSGVQVEGLTVQVILGAPELLGGAE-----PGTYLTGTINGDPESVASL 142
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DB 74 HLKLPDQSGFLAPGFTLQTVGRSP-----GSEAQHLDPGTDLAHCIFYSGTVNGDPGSAAL 129
QY 143 HWDGGALLGVQVRGAELHLOPLEG-----GTP--NSAGGPGAHILRRKSPASQGP 192
DB 130 SLCEG--VRGAFYLGQEEFFIQPAPGATERLAPVPEESSARPQPHILRRRGSG-GA 187
QY 193 MCNV-----KAPLAGSPSPRR-----RAKRPFASLSRFVETL 223
DB 188 KCGWMDDELTPSDSRPESQNTENQVVRDPTQDACKSGSPGSIKRRFVSPPRYETM 247
QY 224 VVADDKMAAFHAGLAKRYLLTMAAAKAFKPSIRNPVSLVTRVLVILSGEGPQVGP 283
DB 248 LVADQSMADPHSGSLKHYLLTFSVAARFYKPSIRNSISLVVVKILVIEEQKGPVTS 307
QY 284 SAAQTLSRCAMQRGINTPDSDPDHFDTAILFTRODLGCVSTCDTLGMDVGTVCDPAR 343
DB 308 NAALTURNFNWKQNSPSDRPEHYDTAILFTRODLGCVSTCDTLGMDVGTVCDPAR 367
QY 344 SCAIVEDDGLQSAFTAHAELGHVFNMLHDSKPCISLNGPLSTRHVMAPVMAHVDPEEP 403
DB 368 SCSEVEDDGLQSAFTAHAELGHVFNMLHDSKPCISLNGPLSTRHVMAPVMAHVDPEEP 426
QY 404 WSPCSARFIITDFLDNGYGHCLLDKPEAPLHLPVTFPGKYDADRQCLTFCGDSRHCPCQL 463
DB 427 WSPCSARFIITDFLDNGYGHCLLDKPEAPLHLPVTFPGKYDADRQCLTFCGDSRHCPCQL 486
QY 464 PPCAALWCSGHLNGHMDLODFNIPOAGGNGPWPWGDCSRTCGGV 523
DB 487 ASTCTTLMCTGTGGLLVLCQTRHFPWADGTSCEGKWCVSKCNKMTDKHFATPVHGSW 546
QY 524 GPMGPWGDCTSRCTCGGVQFSSRDCTRPVPRNGKYCEGRTRFRSCNTEDCPTGSALTFR 583
DB 547 GPMGPWGDCTSRCTCGGVQFSSRDCTRPVPRNGKYCEGRTRFRSCNTEDCPTGSALTFR 606
QY 584 BEQCAAYNHRTDLFKSPGPMWVRYTGVAPODQCKLTQCARALGYVYVLEPRVVDGTP 643
DB 607 BEQCAAYNHRTDLFKSPGPMWVRYTGVAPODQCKLTQCARALGYVYVLEPRVVDGTP 666
QY 644 CSPDSSVCVQGRCIHAGCDRIIGSKKFKDKMVCVCGDGGSCSKSGSPKFRFYGYNNVTI 703
DB 667 CSPDSSVCVQGRCIHAGCDRIIGSKKFKDKMVCVCGDGGSCSKSGSPKFRFYGYNNVTI 726
QY 704 TTPAGATHILVROQGNPGRHS--LYLALKLPDGSVALNGEYTLMPSTDVLPGLVSLRY 761
DB 727 TTPAGATHILVROQGNPGRHS--LYLALKLPDGSVALNGEYTLMPSTDVLPGLVSLRY 785
QY 762 SGATASETLSHGGLAQLTQVLVAGNPQDTRLRYSFVFPRTPTSTPRTPQDMLHRAQIL 818
DB 786 SGATASETLSHGGLAQLTQVLVAGNPQDTRLRYSFVFPRTPTSTPRTPQDMLHRAQIL 843

RESULT 5
US-09-130-491-2
; Sequence 2, Application US/09130491
; Patent No. 6416974
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Goodearl, Andrew D.J.
; TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83
; FILE REFERENCE: 09404/041001
; CURRENT APPLICATION NUMBER: US/09/130,491
; CURRENT FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: US 60/058,108
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: US 60/054,961
; EARLIER FILING DATE: 1997-08-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 967
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-09-130-491-2

Query Match 46.7%; Score 2135; DB 4; Length 967;
Best Local Similarity 49.3%; Pred. No. 1.6e-152;
Matches 415; Conservative 127; Mismatches 226; Indels 70; Gaps 18;

QY 37 LLLLLLASLLPSARLASPLPREBEEIVFPEKINGSVLPGSGAPARLLCRLOAFQETLLEL 96
DB 36 LLLLLAAALLAVSDALGRPSEDEELVPELERA---PGHGT-TRL--RLHAFDQQLDLEL 89
QY 97 EQDSGVQVGLTVQYLGOAPELGGAB---PGT-----YLTGTINGDPSPVASLHWDGGA 148
DB 90 RPDSSFLAPGFTLQNVGRK-----SGSETPLPETDLAHCIFYSGTVNGDPSSAAALSCEG- 144
QY 149 LLGVLYRGAELHQLLEGSTPNSA--GGPGA-----HILRRK----- 184
DB 145 VRGAFYLLGEAYFIQPLPAASERLATAAPEKPPAPLQFHLRLRNQGDVGGTCGVVDDE 204
QY 185 -----SPASQGGPMCNVAP-----LGSPSPRPR--RAKRFASLSRFFVETLV 224
DB 205 PRPTGKAETEDDEGTEGEDEGQWSPQDPALQGVQPTGTSIRKRFVSSHRYVETML 264
QY 225 VADDKMAAFHAGLKRLLYLLTWMAAAKAFKPSIRNPVSLVTRVLVILSGEGEPQVGPS 284
DB 265 VADQSMAEFHGSLKHVLLTLFSAARLYKHPSIRNSVSLVVKILVIHDEQKGPVTSN 324
QY 285 AAGTIRSFCAWQRIANTPDSDPDHTAILFTRODLGVSTCDTLGMADVGTVCDPARS 344
DB 325 AALTIRNFNCWQKHNPSPDRDAEHYDTAILFTRODLGVSTCDTLGMADVGTVCDPARS 384
QY 345 CAIVEDDGLQSAFTAALHGHVFNMLHNSKPCISLNGPLSTRHVMAPVMAHVDPEEPW 404
DB 385 CSVIEDDGLQAAFTTAHELGHVFNMPHDDAKQCASLNG-VNQDSHMAWSMLNLSHPW 443
QY 405 SPCSARFIDTDLNGYCHLLDKPEAPLHPLVTFPGKDYDADRCQCLTFCGDSRHCPQLP 464
DB 444 SPCSAYMITSFLDNGHGECLMDKPNPQLPGLDLPSTYDANRQCOFTFGEDSKHCPDAA 503
QY 465 PPCAALWCSHGLNHGAMCOTKHSPWADGTPCGPAQACMGRCCLHMDQLQDFNIPQAGGWG 524
DB 504 STCSTLWCTGTSGLVLCQTKHFPWADGTSCEGKWCINGKCNKTRKHFDTPFHGSMG 563
QY 525 PMGPWDCSRTCCGGVQVQFSRDCRTPVPNRNGKYCEGRRTRFRSNTEDCPTGSALTFR 584
DB 564 MWGPWDCSRTCCGGVQVQVYTWRECDNVPVKNKGKCEGKRVYRSCNLEDPCDNNKTFRE 623
QY 585 EQCAAYNHRDIL-FKSPFGPMWVPRYTGVAPODCKLTQCARALGYHYVLEPRVDGTP 643
DB 624 EQCEAHNEFSKASFGSGPA-VEWIPKYAGVSPKDRCKLICQAKGIGYFFVLQPKVWDGTP 682
QY 644 CSPDSSVCVQGRCIHAGCDRIIGSKKFKDKMVCVCGDGGSGCSKQSGSFRKRYGNNV 703
DB 683 CSPDSTSVQVQGVQVAGCDRIIDSXKFKDKGVCGGNGSTCKKISGVSPTSAPGVHDI 742
QY 704 TIPAGATHILVROQGNPHRS--IYLALKLPDGSYALNGEYTLMPSPDVLVPCAVSLRY 761
DB 743 TIPTGATNIEVKQRNQRNGSRNNGSFLAKAADGTIYLNGDYTLSTLEQDIMYKGV-LRY 801
QY 762 SGATASETLSGHGPLAQPLTLOVLVAGNPQDTRLYRYSFFVPRPTPS--TPRPTPDWL 818
DB 802 SGSSAALIRSRFSLKEPLTIQVLTVGNALRPKIKYTFVVKKKGESFNAIPTFSAMV 859

RESULT 6

US-09-568-559-2
; Sequence 2, Application US/09568559
; Patent No. 6649377
; GENERAL INFORMATION:
; APPLICANT: Klonowski, Paul
; APPLICANT: Allard, John
; APPLICANT: Heller, Renu
; APPLICANT: Van Wart, Harold
; TITLE OF INVENTION: Human Aggrecanase and Nucleic Acid

; TITLE OF INVENTION: Compositions Encoding the Same

; FILE REFERENCE: ROCH-002
; CURRENT APPLICATION NUMBER: US/09/568,559
; CURRENT FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: 60/133,343
; PRIOR FILING DATE: 1999-05-10
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 949
; TYPE: PRT
; ORGANISM: human
; US-09-568-559-2

Query Match 46.6%; Score 2131; DB 4; Length 949;

Best Local Similarity 49.3%; Pred. No. 3.2e-152;
Matches 416; Conservative 121; Mismatches 226; Indels 80; Gaps 18;

QY 37 LLLLLLASLLPSARLASPLPREBEEIVFPEKINGSVLPGSGAPARLLCRLOAFQETLLEL 96
DB 18 LLLLLAAALLAVSDALGRPSEDEELVPELERA---PGHGT-TRL--RLHAFDQQLDLEL 71
QY 97 EQDSGVQVGLTVQYLGOAPELGGAB---PGT-----YLTGTINGDPSPVASLHWDGGA 148
DB 72 RPDSSFLAPGFTLQNVGRK-----SGSETPLPETDLAHCIFYSGTVNGDPSSAAALSCEG- 126
QY 149 LLGVLYRGAELHQLLEGSTPNSA--GGPGA-----HILRRKSPASQGGPMCNVAP 199
DB 127 VRGAFYLLGEAYFIQPLPAASERLATAAPEKPPAPLQFHLRLRNQGD-VGGTCGVV-- 183
QY 200 LGSPSPRPR-----DDEPRPTGKAETEDDEGTEGEDEGAQWSPQDPALQGVQPTGTSIRKRFVSSHRY 241
DB 184 --DDEPRPTGKAETEDDEGTEGEDEGAQWSPQDPALQGVQPTGTSIRKRFVSSHRY 241
QY 220 VETLVVADDKMAAFHAGLKRLLYLLTWMAAAKAFKPSIRNPVSLVTRVLVILSGEGEP 279
DB 242 VETMLVADQSMAEFHGSLKHVLLTLFSAARLYKHPSIRNSVSLVVKILVIHDEQKGP 301
QY 280 QVGPSSAAQTLRSFCWQRIANTPDSDPDHTAILFTRODLGVSTCDTLGMADVGTVC 339
DB 302 EVTSNAALIRNFNCWQKHNPSPDRDAEHYDTAILFTRODLGVSTCDTLGMADVGTVC 361
QY 340 DPARSACAIVEDDGLQSAFTAALHGHVFNMLHNSKPCISLNGPLSTRHVMAPVMAHVD 399
DB 362 DPSRSCSVIEDDGLQAAFTTAHELGHVFNMPHDDAKQCASLNG-VNQDSHMAWSMLNLD 420
QY 400 PEEPWSPCSARFIDTDLNGYCHLLDKPEAPLHPLVTFPGKDYDADRCQCLTFCGDSRH 459
DB 421 HSQPMWSPCSAYMITSFLDNGHGECLMDKPNPQLPGLDLPSTYDANRQCOFTFGEDSKH 480
QY 460 CPQLPFPCCALWCSHGLNHGAMCOTKHSPWADGTPCGPAQACMGRCCLHMDQLQDFNIPQ 519
DB 481 CPDAASTCSTLWCTGTSGLVLCQTKHFPWADGTSCEGKWCINGKCNKTRKHFDTPF 540
QY 520 AGGWGPWGPWDCSRTCCGGVQVQFSRDCRTPVPNRNGKYCEGRRTRFRSNTEDCPTGSA 579
DB 541 HGSXGMPWGPWDCSRTCCGGVQVQVYTWRECDNVPVKNKGKCEGKRVYRSCNLEDPCDNNNG 600
QY 580 LTPREQCAAYNHRDIL-FKSPFGPMWVPRYTGVAPODCKLTQCARALGYHYVLEPRV 638
DB 601 KTFREQCEAHNEFSKASFGSGPA-VEWIPKYAGVSPKDRCKLICQAKGIGYFFVLQPKV 659
QY 639 VDGTPCSPDSSVCVQGRCIHAGCDRIIGSKKFKDKMVCVCGDGGSGCSKQSGSFRKPRYG 698
DB 660 VDGTPCSPDSTSVQVQGVQVAGCDRIIDSXKFKDKGVCGGNGSTCKKISGVSPTSAPGV 719
QY 699 YNNVVTIPAGATHILVROQGNPHRS--IYLALKLPDGSYALNGEYTLMPSPDVLVUPGA 756
DB 720 YHDIITPTGATNIEVKQRNQRNGSRNNGSFLAKAADGTIYLNGDYTLSTLEQDIMYKGV 779
QY 757 VSLRYSGATASETLSGHGPLAQPLTLOVLVAGNPQDTRLYRYSFFVPRPTPS--TPRPTPQ 815
DB 780 V-LRYSGSSAALIRSRFSLKEPLTIQVLTVGNALRPKIKYTFVVKKKGESFNAIPTFS 838

QY 816 DWL 818
Db 839 AWV 841

RESULT 7
US-09-445-023A-1
; Sequence 1, Application US/09445023A
; Patent No. 6565858
; GENERAL INFORMATION:
; APPLICANT: Hirose, Kunitaka
; APPLICANT: Inoguchi, Eiichi
; APPLICANT: Hakozaaki, Michinori
; APPLICANT: Ishioka, Keiko
; APPLICANT: Ishida, Yukako
; APPLICANT: Matsushima, Kouji
; APPLICANT: Kuno, Kouji
; TITLE OF INVENTION: Human ADAMTS-1 protein, gene encoding the same, pharmaceutical
; FILE REFERENCE: Q57092
; CURRENT APPLICATION NUMBER: US/09/445, 023A
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: JP 9-160422
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 727
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-445-023A-1

Query Match 43.7%; Score 1998.5; DB 4; Length 727;
Best Local Similarity 57.5%; Pred. No. 2.2e-142;
Matches 353; Conservative 105; Mismatches 149; Indels 7; Gaps 6;

QY 209 RAKRFASLSRFVETLVVADDDKMAAFHAGLKRLLYLVMAAAKAFKHPISIRNPVSLVVR 268
Db 9 RKRFVSSPRVYETMLVADQSMALFSGGLKHYLLTLFVVAARLYKHPISIRNSVSLVVVK 68

QY 269 LVILGSGEGPQVPSAAOTLRSFCWQRLNTPEDSDPDHFTALFTRODLGCVSTCD 328
Db 69 ILVHDEQKGPVETSNALTLRNFQWQHNPSPDRDAEHYDTALFTRODLGCVSTCD 128

QY 329 TLGMADVGTCDPARSCAIVEDDGLQSAFTAAHGLHGVNMLHDSKPCISLNGPLSTR 388
Db 129 TLGMADVGTCDPSRSCSVIEDDGLQAAFTTAHELGHVFNMPHDDAKQASLNG-VNQDS 187

QY 389 HVMAPYMAHVDPPEEPSPCSARFITDPLDNGYGHCLLDKPEAPLHLPVTPFGKDYDADRQ 448
Db 188 HWASMLNLSHSPWSPCSAYMITSLDNGHGECLMDKFPQNPQLPGDLPGTLYDANRQ 247

QY 449 QLTFGPDSRHCPQLPPPCAAWCSGHLNGHAWCOTKHSFADGTGCGPAQACMGRCULH 508
Db 248 CQTFGEDSKHCPDAASTCTLWCTGTSGVLVVCQTKHFPWADGTSCGEGKWCINGKCVN 307

QY 509 MDQLQDFNTPQAGGWPWPGWDCSRTCGGVQFSSRDCTRPVPRNGKYCEGRTFRPS 568
Db 308 KTDKHFDTFFHGSWGPWPGWDCSRTCGGVQYTWRECDNVPVKNKKYCEGKRVYRS 367

QY 569 CNTEDCPTGSALTFFREEQCAAVNHRDLDL-FKSPFGPMVPRYTGVAPODQCKLTCQARA 627
Db 368 CNLEDCPDNNGKTFREEQCAHNEFSAFSGSPA-VENIPKYAGVSPKDRCKLICQAKG 426

QY 628 LGYVYVLEPRVVDGTPCSPDSSVSVQVQRCIHAGCDRIIGSKKPKDKMVCVCGDGGCSK 687
Db 427 IGYVFFVLQPKVVDGTPCSPDSTSVQVQCVKAGCDRIIDSKKPKDKVCGVCGSGTCKK 486

QY 688 QSGSFRKFRYGYNVVTIPAGATHILVRQGNPHGRS--IYLALKLPDGSYALNGEYTLN 745
Db 487 ISGSVTSAPKGVHDIVTIPTGATNIEVKQRNQRSGRNGSFLAIKAADGTLYLNGDYTLN 546

QY 746 PSPTDVVLFAGVSLRYSGATAASETLSGHGPIAQLPTLQVLVAGNQDTRLRYSFVPRP 805
Db 547 TLEQDIMYKGVV-LRYSGSSAALERIRSPSLKEPLTIQVLTGVGNALRPKIKYTFVKKK 605

QY 806 TFS-TPRTPPDWL 818
Db 606 KESFNAIPTFSAWV 619

RESULT 8
US-09-445-023A-12
; Sequence 12, Application US/09445023A
; Patent No. 6565858
; GENERAL INFORMATION:
; APPLICANT: Hirose, Kunitaka
; APPLICANT: Inoguchi, Eiichi
; APPLICANT: Hakozaaki, Michinori
; APPLICANT: Ishioka, Keiko
; APPLICANT: Ishida, Yukako
; APPLICANT: Matsushima, Kouji
; APPLICANT: Kuno, Kouji
; TITLE OF INVENTION: Human ADAMTS-1 protein, gene encoding the same, pharmaceutical
; FILE REFERENCE: Q57092
; CURRENT APPLICATION NUMBER: US/09/445, 023A
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: JP 9-160422
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 727
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-445-023A-12

Query Match 43.5%; Score 1986; DB 4; Length 727;
Best Local Similarity 56.1%; Pred. No. 2e-141;
Matches 348; Conservative 111; Mismatches 155; Indels 6; Gaps 5;

QY 203 PS-PRPRAKRFASLSRFVETLVVADDDKMAAFHAGLKRLLYLVMAAAKAFKHPISIRNP 261
Db 2 PSQSGSIRKRVSSPRVYETMLVADQSMADFHGSLKHYLLTLFVVAARLYKHPISIRNS 61

QY 262 VSLVTRLVILGSGEGPQVPSAAOTLRSFCWQRLNTPEDSDPDHFTALFTRODL 321
Db 62 ISLVVKKILVYEEQKGPVETSNALTLRNFQWQHNPSPDRDAEHYDTALFTRODL 121

QY 322 CGVSTCDTLGMADVGTCDPARSCAIVEDDGLQSAFTAAHGLHGVNMLHDSKPCISLN 381
Db 122 CGSHTCDTLGMADVGTCDPSRSCSVIEDDGLQAAFTTAHELGHVFNMPHDDAKHCASLN 181

QY 382 GPLSTSRHVPMAHVDPPEEPSPCSARFITDPLDNGYGHCLLDKPEAPLHLPVTPFGK 441
Db 182 G-VSGDHLMAWMLSLDHSQWSPCSAYMVTSLDNGHGECLMDKFPQNPQLPSDLPGT 240

QY 442 DYDADRCQCLTGPDSRHCPQLPPPCAAWCSGHLNGHAWCOTKHSFADGTGCGPAQAC 501
Db 241 LYDANRQCLTGPDSRHCPQLPPPCAAWCSGHLNGHAWCOTKHSFADGTGCGPAQAC 300

QY 502 MGRCLHMDQLQDFNTPQAGGWPWPGWDCSRTCGGVQFSSRDCTRPVPRNGKYCEG 561
Db 301 VSGKCVNKTDMKHFAFPVHGSWGPWPGWDCSRTCGGVQYTWRECDNVPVKNKKYCEG 360

QY 562 RTRFRSCNTECPGSAITFFREEQCAAVNHRDLDL-FKSPFGPMVPRYTGVAPODQCKL 621
Db 361 KEVRYRSCNIEDCPDNNGKTFREEQCAHNEFSAFSGSPA-VENIPKYAGVSPKDRCKL 420

QY 622 TCQARALGYVYVLEPRVVDGTPCSPDSSVSVQVQRCIHAGCDRIIGSKKPKDKMVCVCGD 681
Db 421 TCQARALGYVYVLEPRVVDGTPCSPDSTSVQVQCVKAGCDRIIDSKKPKDKVCGVCGG 480

QY 682 GSGCSKQSGSFRKFRYGYNVVTIPAGATHILVRQGNPHGRS--IYLALKLPDGSYALN 739

481	GSTCKMGSIVTSTRPGVHDIVTTPAGATNIEVKHNRGSRNNGSFLAIRAADGTYILN	540
Db		
740	GYVTLMPSPDVLVLCAYSLKYGATAASELTSGHGLAQLPTLQVLVAGNPQDTRLYS	799
Qy		
541	GNFTLSTLEQDLYTKGV-LVYSGSSAALERISFSLKEPLTQVLVMGHALRPKIKT	599
Db		
800	FFVPRPTPS-TPRPTPDWL	818
Qy		
600	YFWKKKTESFNAIPTFSEW	619
Db		

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RESULT 9
US-10-009-332-1
; Sequence 1, Application US/10009332
; Patent NO. 6711613
; GENERAL INFORMATION:
; APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.
; APPLICANT: Kazusa DNA Research Institute
; TITLE OF INVENTION: NOVEL METALLOPROTEASE HAVING AGGREGANASE ACTIVITY
; FILE REFERENCE: Q67541
; CURRENT APPLICATION NUMBER: US/10/009,332
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: JPA Hei 11-321740
; PRIOR FILING DATE: 1999-11-11
; PRIOR APPLICATION NUMBER: JPA 2000-144020
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 950
; TYPE: ERT
; ORGANISM: Homo sapiens
US-10-009-332-1

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Query Match	41.9%	Score	1917	DB	4	Length	950
Best Local Similarity	46.3%	Pred. No.	4.5e-136				
Matches	381	Conservative	123	Mismatches	267	Indels	52
Gaps							
QY	37	LLLLLLASLPSARLAGPLPREBEIVFEKINGSVL-----PGSGAPARLLCRLOAQF	88				
Db	1	MLLLGILTLAFAGTAGGFEFEREYVVPILRDLINGRRYYWRGPEDSGDGLIFQITAF	60				
QY	89	GETLLLELQDSGVQVQEGTLVQYIQAPE-LLGAEP--GYTLTGTINGDESVASLHWD	145				
Db	61	QEDFVYLHTPDQAQFLAPAFSTEHLGVPLQGLTGSSDLRRCFYSGDVNAEPDPSAAVSLC	120				
QY	146	GGALLGVLYQGAELHLOPLEGGTPNSA--GPGGAHILRRK-----SPASGGQPMCNV---	196				
Db	121	GG-LRGAFYQGAEEYVISPLPNASAPQAQRNSQGAHLLQRRGVPGGSGDPTSRGCVASG	179				
QY	197	-----KAPLGSPSPRPR--RAKRFASLSRFVETLVVADDKMAAFHGAGLK	239				
Db	180	WNPAILRALDPYKPRRAGFESRRSRGAKRFVSIPIRYVETLVVADESVMKHFHADLE	239				
QY	240	RYLLTWMAAAKAFKHPISIRNPVSLVTRVLVILSGSEEGPQVGPSSAAOTILSFCMAORGL	299				
Db	240	HYLLTLLTAARLYRHPISILNPINIVVVKVLLLRDRDGPVKVTGNAULTLRFCAWKKL	299				
QY	300	NTPEDSDPHFDTALFTFRQDLGVSTCDTLGMADVGTVCOPARCAIVEDDGLQSAFTA	359				
Db	300	NKVSXKHEPYMDTALFTFRQDLCGAHTCDTLGMADVGTWMDPKRSCSVIEDDGLPSAFTT	359				
QY	360	AHELGHVFNMLHDSKPCISLNGPLSTSRHVNAPVMVHVDPPEMSPCSARFITDFLONG	419				
Db	360	AHELGHVFNMPHDNVKVCVEVPGLK-RANHHMSPTLIQIDRANPWSACSAAIITDFLDG	418				
QY	420	YGHCLLDKPEAPLHLPTVTFPGKDYADRCOLTFGPDSRHCPQLPQPPCAALWCSGHLNCH	479				
Db	419	HGDCILLDPFSKPISUPEDLFGASYYTLQSQCELAFGVGSKPCPYM-QYCTKLWCTGKAKGQ	477				
QY	480	AMCQTKHSPWADGTPCGFAQAQCGWRGCLHMDQLQDFNIPQAGWGVPWGPWGDCSRTCGGG	539				

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Db      478  MVCQTRHPWADGTSCEGKCLKKGACVERHNLNKRVD--GSWAKWDPYGPCSRTCQGG 535
Qy      540  VQSSRDCTRPVRNGKCYCEGRTRFRSCNTEDCP-TGSALTFRBOCAA---YNHRTD 595
Db      536  VQLARRQCTNPTPANGKCYCEGVRVKYRSCNLEPCFSPSSAGSKSFRBOCEAFNGYNHSTN 595
Qy      596  LFKSFFQPMDWPRYTGVAPODOCKLTCOARALGYVYVLEPRVVDGTPCSPDSSSVCVQG 655
Db      596  RLTL---AVAWPKYSGVSPRDKCKLICRANGTGYFVLAPKVVDGTLCSPDSTSVCVQG 652
Qy      656  RCIHAGCDRIIGSKKPKDKCMVCGDPSGCSKQSGFRKFRYGYNNVVTIPAGATHILVR 715
Db      653  KCIKAGCDGNLGSKGRFCKGCVCGDGNKSCCKVTGLTKPMHGYNFYVAIPAGASSIDIR 712
Qy      716  QQGNPG--HRSIYIALKLPDGSYALNAGEYTLMPSTDVVLPGAVSLRYSGATAASETLSG 773
Db      713  QRYGKGLIGDNDYALAKNSGKYLNLGHFVVSAVERDLVVKGSL-LRYSGTGTAVESLOA 771
Qy      774  HGPLAOPLTQLVLVAGNPQDTRLRYSFVFPVPRTPSTPRTPQD 816
Db      772  SRPILEPLTVEVLVSGKMTFPRVRYSPFLPKPEKREDKSSHPKD 814

RESULT 10
US-09-369-364A-9
; Sequence 9, Application US/09369364A
; Patent No. 6391610
; GENERAL INFORMATION:
; APPLICANT: Aptec, Suneel
; APPLICANT: Hurskainen, Tiina L.
; APPLICANT: Hirohata, Satoshi
; TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
; FILE REFERENCE: 26473/4007/10-30-00
; CURRENT APPLICATION NUMBER: US/09/369,364A
; CURRENT FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 905
; TYPE: PRT
; ORGANISM: Mus musculus ADAMTS-8
; US-09-369-364A-9

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Query Match	39.9%;	Score 1824;	DB 3;	Length 905;	
Best Local Similarity	44.2%;	Pred. No. 4.5e-129;			
Matches 373;	Conservative 134;	Mismatches 233;	Indels 104;	Gaps 26	
QY	36	WLLLLLLASLLPSARLASPLP-----RREIIVPEKLGSLVLP	PGSGAPARLLCRLQAF	88	
DB	10	WPPLLLLLLQLPPPPPLVCGAPAGCTGAQSELVVP	TRLPGSA	62	
QY	89	GETLLLELQDSGVQVEGLTVQYLGOAPELLGGAEP--	GTVLTCGTINDPDESVAASHL--	143	
DB	63	GGFVRLRAPDASFLAPBEKRIELGGSSAAAGG-EP	GLRGCFSTVNGERESLAAMSCV	121	
QY	144	--WDGGALLGVLYQRGASLHLQPLEGG---TPN--	SAGGPGCAHLRRKSP-----	186	
DB	122	AGWSGSFLLA-----GEFTTQPQAGDSLQDP	PHLQRWGPGQ---RRDPGLAAAEVFP	173	
QY	187	-----ASGGG-----	PMCNVKAPLGSPSPRPRAKRF	213	
DB	174	LPQGLEWEVMGNGGQGSERNEEDKKQKEGLLK	ETEDSRKVPFPFGSKT-----RSKRF	229	
QY	214	ASLSRFVETLVADDKMAAFHCGAGLKR	YLLTWMAAAAKAFKHPSTENP	VSLLVVTURLVILG	273
DB	230	VSEARFVETLVADASMAAFYGTDLQNHLL	TVMGSMARIRYKHPSIRNS	VNLVVVKVLIVE	289
QY	274	SCEEGPQVGPSAAQTLRSFCAWORGLNTP	EDSDPHFDTAILLFTFRQDL	LCGV--STCDTLGM	332
DB	290	KERWGPFEVSDNGGLTRLRFCSWQRFRN	PSDRHPHYDTAILFTFQNF	CGKGEQCDTLGM	349
QY	333	ADGVVTCVDPARSCAIVEDDGLQSAF	ATAAHLGHVFNMHLHNSKPCISL	NGPLSTSRHVNA	392

Db 350 ADVGTICDPKSCSVIKDGLQAQYTLAHLGHVLSMPHDDKPCVRLFGPMG-KYHMA 408
 QY 393 PYMAHVDPPEPSPCSAREITFDNGYGHCLLDKPEALPLHLPVTPPGKD--YDADROCO 450
 Db 409 PFFIHWKTLWSPSCSAVYLTLLDGHGCLLDAPTSVLPPLTGLPGHSTIYELDQCK 468
 QY 451 LTFGDSRHCP--QLPPPCAALWCSGHLNG-HAMCOTKSP--WADGTPCGPAQACMGOR 505
 Db 469 QIFGDPFRHCPNTSVBEDIQVL-CARHRSDDEPICHTKNGSLIADWDTGCPGPHLCIDGS 527
 QY 506 CLHMOLOQFNIPQAGGWPWPGWDCSRTCGGVQVQSSRDCTRPVPRNGKCYCEGRTR 565
 Db 528 CVLKEDVENKAVVDGWPWPGWDCSRTCGGVQVQSSRDCTRPVPRNGKCYCEGRTR 587
 QY 566 FRSCNTEDCPTGSALTFRREEQCA--AYNHRITDLFKSPGPMWVPRYTGVAPODOCKLT 622
 Db 588 YQSCNTEECPP-NGKSFREQCEKYNVNH-TDLGNF--LQWPKYSGVSPDRCKLF 642
 QY 623 COARALGYVYVLEPRVVDGTPCSPDSSSVQVQRCIHAGCDRIIGSKKFKDKMVCVGGDG 682
 Db 643 CRARGRSEBKFVPEAKVIDGTGLGPDPTLSICVRGQCVKAGCDHVNWSPKLDKCGVCGGKG 702
 QY 683 SCSCSOGSFRFRYGNVNVITIPAGATHILVROQGNPGHRS--IYLALKLPDGSYALNG 740
 Db 703 TACRKISGTFPSGYNDIVITIPAGATNIDVKORSHPGVRNDGSYALKTANGQYLLNG 762
 QY 741 EYTLMPSPDVLPGAVSLRYSGATAASETLSGHGPLAQLTLQVL-VAGNPQDTRLRYS 799
 Db 763 NLAISAEQDILVKGTI-LKYSGMTALRLQSFQALPELTLVQLLTVSGEVFPKRYT 821
 QY 800 FVFP 803
 Db 822 FVFP 825

RESULT 11
 US-09-130-491-13
 ; Sequence 13, Application US/09130491
 ; Patent No. 6416974
 ; GENERAL INFORMATION:
 ; APPLICANT: Holtzman, Douglas A.
 ; APPLICANT: Goodearl, Andrew D.J.
 ; TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83
 ; FILE REFERENCE: 09404/041001
 ; CURRENT APPLICATION NUMBER: US/09/130,491
 ; CURRENT FILING DATE: 1998-08-07
 ; EARLIER APPLICATION NUMBER: US 60/058,108
 ; EARLIER FILING DATE: 1997-09-05
 ; EARLIER FILING DATE: 1997-08-06
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 13
 ; LENGTH: 608
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-09-130-491-13

Query Match 39.2%; Score 1793.5; DB 4; Length 608;
 Best Local Similarity 56.5%; Pred. No. 5.3e-127;
 Matches 313; Conservative 97; Mismatches 137; Indels 7; Gaps 6;
 QY 269 LVLSGEGGPOVGPAAOTLRSFCAWQGLNTPEDSDPHFDTALTFRQDLGCVSTCD 328
 Db 4 ILVIHDEQKGPVTSNAALTILNFCWQKHPPSPDRDAEHVDTALTFRQDLGCVSTCD 63
 QY 329 TLGMADVGTCDPARSCAIVDDGLQSAFTAHAHLGHVFNMLHNSKPCISLNGPLSTR 388
 Db 64 TLGMADVGTCDPSRSCSVIEDGLQAFTTAHLGHVFNMPHDDAKQACASLNG-VNQDS 122
 QY 389 HWAPFWMHVDEEPWSPSCSAFITDNLNGYGHCLLDKPEALPLHLPVTPPGKDADQ 448
 Db 123 HWMASLNLDSQWSPSCSAFYMTISFLDNGHGECLMDKPNQPIQLPGDLPGTSYDANRQ 182

QY 449 COLTRGPDSSRHCPQLPPPCAALWCSGHLNGHAMCOTKHSFPWADGTPCGPAQACMGRCILH 508
 Db 183 COFTFGEDSKHCPDAASTCTSLWCTGSGVLVCQTKHFPWADGTCGEGKWCINGKCVN 242
 QY 509 MDLOLOQFNIPQAGGWPWPGWDCSRTCGGVQVQSSRDCTRPVPRNGKCYCEGRTRFRS 568
 Db 243 KTDKRFHDFPFGSGWGMWPGWDCSRTCGGVQVQSSRDCTRPVPRNGKCYCEGRTRFRS 302
 QY 569 CNTEDCPTGSALTFRREEQCAAYNHRITDL-FKSPGPMWVPRYTGVAPODOCKLTQCARA 627
 Db 303 CNLEDCPDNNGKTFREEQCEAHNEFSKASFGGPA-VEMIPKTAGVSPDKRCKLIQAKG 361
 QY 628 LGYVYVLEPRVVDGTPCSPDSSSVQVQRCIHAGCDRIIGSKKFKDKMVCVGGDGSCSK 687
 Db 362 IGYVYVLEPRVVDGTPCSPDSSSVQVQRCIHAGCDRIIGSKKFKDKMVCVGGDGSCSK 421
 QY 688 QSGSRFRFRYGNVNVITIPAGATHILVROQGNPGHRS--IYLALKLPDGSYALNGEYTL 745
 Db 422 ISGSVTSAPKGYHDIITIPAGATNIEVKQNRQSGRNGSFLAIAKADGTIILNGDYTL 481
 QY 746 PSPTDVLPGAVSLRYSGATAASETLSGHGPLAQLTLQVLVAGNPQDTRLRYSFVPRP 805
 Db 482 TLEQIMYKGV-LRYSGSSAALRLRSPSLKEPLTIQVLTGVNLRPKIKITIFVKKK 540
 QY 806 TPS-TPRPTPDWL 818
 Db 541 KESFNAIPTFSAW 554

RESULT 12
 US-09-369-364A-2
 ; Sequence 2, Application US/09369364A
 ; Patent No. 6391610
 ; GENERAL INFORMATION:
 ; APPLICANT: Apte, Suneel
 ; APPLICANT: Hurskainen, Tiina L.
 ; APPLICANT: Hirohata, Satoshi
 ; TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
 ; FILE REFERENCE: 26473/4007/10-30-00
 ; CURRENT APPLICATION NUMBER: US/09/369,364A
 ; CURRENT FILING DATE: 1999-08-06
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 930
 ; TYPE: PRT
 ; ORGANISM: mus musculus ADAMTS-5
 US-09-369-364A-2

Query Match 34.5%; Score 1576; DB 3; Length 930;
 Best Local Similarity 39.1%; Pred. No. 2.5e-110;
 Matches 348; Conservative 127; Mismatches 301; Indels 114; Gaps 22;
 QY 31 LSW--LWMLLLLLSL--PSARLASPLP-----RREIV 62
 Db 3 LEWASILLLLLLSLAADSAPAAPOKTRQPAQAAAAAEPDQPGERTREGRHL 62
 QY 63 FP---EKLNGSVL-----PGSGAPARLLCRLOAFGETLLELEODSGVQVGLTVQYL 112
 Db 63 QPLAQRRSGGIVHNDIQLYSGGKGVYL---VYAGRRFLDLDERDDTVGAAG-SIVTA 118
 QY 113 GQAPELLGABEPTVLTGTINGDPESVASLHWDGALLGVQVRGAELHQLPEGG--- 168
 Db 119 GGLSASSGHRGHCYRGTVDSPLAVDFLCGG-LDGFVAVKHARYTLKPLLRGSWAE 177
 QY 169 -----TPNSAGG-----PGAHI-LRRKSPASGQ 190
 Db 178 YERIYGDGSSRIILHVNRGFGFEALPPRASCETPASPSPQSPSVHSRRRSALAPQ 237
 QY 191 GPMCNVAPLGPSPSRP--RRAKRRFASLRFVETLVVADDKMAAFHAGLKRILLTMAA 248
 Db 238 LLDHSAFSPSGNAGPQTWRRRRRSISRARQVELLLVADSSMARMYGRGLHYLLTMAI 297

Best Local Similarity 41.2%; Pred. No. 5.6e-109;
Matches 325; Conservative 120; Mismatches 258; Indels 85; Gaps 19;

QY 87 AFGEITLLELEODSGVQVEGLTVQVILGQAPPELLGGAEP-----GTYLITTINGDPSVAS 141
Db 93 AGGRFLDLDERDGSVGIAGF-----VPAGGTSAPWRHSHCFYRGTVGDASPRSLAV 145
QY 142 LHWGCGALLGVLYQVGAELHLOPLEGG----- 168
Db 146 FDLGG-LDGFPAVKHARYTLKPLLRGPWABEKGVRVYGGGSARILHVVYTBREGFSPEALP 204
QY 169 -----TPNSAGGPGAHILRRKSPA-----SGQGPC-----NVKAPLSPSPRP--RRA 210
Db 205 PRASCETP--ASTPEAH-----EHAPAHNSPNSGRAALASQLLDQSALSPPAGSGPQTWRRR 259
QY 211 KFPASLSRPFVETLVVADDDKMAAFHAGLKYLLTWMAAAKAFKHPISINPVSLLVTVLV 270
Db 260 RASISRARQVELLLVADASMARLYGRGLQHYLLTLASIANRLYSHASINHLRLAVKVV 319
QY 271 ILGSEBEGPQVGPSSAAQTLRSFCAWORGLNTPEDSDPHDFTAILFTRODLGCVSTCDTL 330
Db 320 VLGDKDKSLEVSCKNAATLLKNFKWQHONQDDEEHYDAALLFTREDLCGHSCDYL 379
QY 331 GMADVTCDDPARSCAIVDDGLQSAFTAAHGLHGVNMLHNSKPCISLNGPLSTSRHV 390
Db 380 GMADVTCISPSRSCAVIEDDGLHAAFTVAHEIGHLLGLSHDSDSKFCEETFGSTEDKR-L 438
QY 391 MAPVMAHVDPPEPWPSCSARFTDFLDNGYGHCLLDKPEAPLHLPVTFPGKYDADROCC 450
Db 439 MSILTSIDASKPWSKCTSATITEFLDDGHGNCLLDLPRKQILGPBELPGQTYDATQCCN 498
QY 451 LTFGPDSPHCPOLPPPCAAALWCSHNLGHAMCOTKHSFWADGTPCGPAQACMGRCCLHMD 510
Db 499 LTFGEYSVCPGM-DVCARLWCAVVRQGMVCLTKKLPAVEGTPCKGRIKLOGKCVDTK 557
QY 511 QIQDNFIPOAGWGPMPGDCSRTCGGVQFSSRDCTRPVPRNGGKYCEGRTRFRSCN 570
Db 558 KKKYTSSTSHGNWGSWGSQCSRSQCGGVQPAYRHCNNPAPRNNGRYCTGKRAIYRSCS 617
QY 571 TEDCTGSALTREBOCAAYN-HRTDL--FKSPFGPMWVRYTGVAPODCKLTQCARA 627
Db 618 LMPCPP-NGKSPRHOCEAKNGYQSDAKGVKTF---VEWVPKYAGVLPADVCKLTCKRAG 673
QY 628 LGYVYVLEPRVVDGTPCSPDSSVQVGRICIHAGCDRIIGSKKKFKCMVCGDGGSGCSK 687
Db 674 TGYVYVFPKVTGTECRYSNVSVRGKCVRTGCDIIGSKLOYDKCGVCGDSSCTK 733
QY 688 QSGSFRKFRYGNVNVVITIPAGATHILVRO--QGNPGHRSIYLALKLPDGSYALNGEYTL 745
Db 734 IVGTENKSKGYTDVVRIPEGATHIKVROFKAKDQTRFTAYLALKKKNGEYLINGKYMIS 793
QY 746 PSPTDVLPGVSLRYSGATASETLSHGGLA--OPLTLQVLVAGNPDTRLRYSFFVP 803
Db 794 TSETIIDINGTV-MNYSWMSHRDDFLHGMGYSATKEILIVQILATDPTKPLDVRYSFFVP 852
QY 804 RPTPSTPR 811
Db 853 K--KSTPK 858

Search completed: April 1, 2005, 12:33:57
Job time : 49 secs

QY 142 LHWGCGALLGVLYQVGAELHLOPLEGG----- 168
Db 146 FDLGG-LDGFPAVKHARYTLKPLLRGPWABEKGVRVYGGGSARILHVVYTBREGFSPEALP 204
QY 169 -----TPNSAGGPGAHILRRKSPA-----SGQGPC-----NVKAPLSPSPRP--RRA 210
Db 205 PRASCETP--ASTPEAH-----EHAPAHNSPNSGRAALASQLLDQSALSPPAGSGPQTWRRR 259
QY 211 KFPASLSRPFVETLVVADDDKMAAFHAGLKYLLTWMAAAKAFKHPISINPVSLLVTVLV 270
Db 260 RASISRARQVELLLVADASMARLYGRGLQHYLLTLASIANRLYSHASINHLRLAVKVV 319
QY 271 ILGSEBEGPQVGPSSAAQTLRSFCAWORGLNTPEDSDPHDFTAILFTRODLGCVSTCDTL 330
Db 320 VLGDKDKSLEVSCKNAATLLKNFKWQHONQDDEEHYDAALLFTREDLCGHSCDYL 379
QY 331 GMADVTCDDPARSCAIVDDGLQSAFTAAHGLHGVNMLHNSKPCISLNGPLSTSRHV 390
Db 380 GMADVTCISPSRSCAVIEDDGLHAAFTVAHEIGHLLGLSHDSDSKFCEETFGSTEDKR-L 438
QY 391 MAPVMAHVDPPEPWPSCSARFTDFLDNGYGHCLLDKPEAPLHLPVTFPGKYDADROCC 450
Db 439 MSILTSIDASKPWSKCTSATITEFLDDGHGNCLLDLPRKQILGPBELPGQTYDATQCCN 498
QY 451 LTFGPDSPHCPOLPPPCAAALWCSHNLGHAMCOTKHSFWADGTPCGPAQACMGRCCLHMD 510
Db 499 LTFGEYSVCPGM-DVCARLWCAVVRQGMVCLTKKLPAVEGTPCKGRIKLOGKCVDTK 557
QY 511 QIQDNFIPOAGWGPMPGDCSRTCGGVQFSSRDCTRPVPRNGGKYCEGRTRFRSCN 570
Db 558 KKKYTSSTSHGNWGSWGSQCSRSQCGGVQPAYRHCNNPAPRNNGRYCTGKRAIYRSCS 617
QY 571 TEDCTGSALTREBOCAAYN-HRTDL--FKSPFGPMWVRYTGVAPODCKLTQCARA 627
Db 618 LMPCPP-NGKSPRHOCEAKNGYQSDAKGVKTF---VEWVPKYAGVLPADVCKLTCKRAG 673
QY 628 LGYVYVLEPRVVDGTPCSPDSSVQVGRICIHAGCDRIIGSKKKFKCMVCGDGGSGCSK 687
Db 674 TGYVYVFPKVTGTECRYSNVSVRGKCVRTGCDIIGSKLOYDKCGVCGDSSCTK 733
QY 688 QSGSFRKFRYGNVNVVITIPAGATHILVRO--QGNPGHRSIYLALKLPDGSYALNGEYTL 745
Db 734 IVGTENKSKGYTDVVRIPEGATHIKVROFKAKDQTRFTAYLALKKKNGEYLINGKYMIS 793
QY 746 PSPTDVLPGVSLRYSGATASETLSHGGLA--OPLTLQVLVAGNPDTRLRYSFFVP 803
Db 794 TSETIIDINGTV-MNYSWMSHRDDFLHGMGYSATKEILIVQILATDPTKPLDVRYSFFVP 852
QY 804 RPTPSTPR 811
Db 853 K--KSTPK 858

RESULT 15
US-10-247-685-15
; Sequence 15, Application US/10247685
; Patent No. 6753176
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: AGGREGAN DEGRADING METALLO PROTEASES
; FILE REFERENCE: DM6909D
; CURRENT APPLICATION NUMBER: US/10/247,685
; CURRENT FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 930
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-247-685-15

Query Match 34.1%; Score 1558; DB 4; Length 930;

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 12:30:41 ; Search time 149 Seconds
(without alignments)
1862.706 Million cell updates/sec

Title: US-09-634-287E-2

Perfect score: 4570

Sequence: 1 MSQTGSHPGRLAGRWLWGA.....LHRRQAQILRRRPWAGRK 837

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1413372 seqs, 331592847 residues

Total number of hits satisfying chosen parameters: 1413372

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
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8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
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19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	4570	100.0	837	14	US-10-247-685-2
2	4570	100.0	837	16	US-10-408-785A-1348
3	4570	100.0	837	16	US-10-628-432-1
4	4567	99.9	846	16	US-10-628-432-29
5	4566	99.9	837	15	US-10-358-283-11
6	4563	99.8	837	10	US-09-946-374-317
7	4563	99.8	837	13	US-10-052-586-352
8	4563	99.8	837	14	US-10-174-590-352
9	4563	99.8	837	14	US-10-176-758-352
10	4563	99.8	837	14	US-10-175-737-352
11	4563	99.8	837	14	US-10-174-581-352
12	4563	99.8	837	14	US-10-176-483-352
13	4563	99.8	837	14	US-10-176-749-352
14	4563	99.8	837	14	US-10-176-749-352

14	4563	99.8	837	14	US-10-176-914-352	Sequence 352, App
15	4563	99.8	837	14	US-10-176-915-352	Sequence 352, App
16	4563	99.8	837	14	US-10-173-706-352	Sequence 352, App
17	4563	99.8	837	14	US-10-175-738-352	Sequence 352, App
18	4563	99.8	837	14	US-10-175-752-352	Sequence 352, App
19	4563	99.8	837	14	US-10-176-482-352	Sequence 352, App
20	4563	99.8	837	14	US-10-176-757-352	Sequence 352, App
21	4563	99.8	837	14	US-10-176-913-352	Sequence 352, App
22	4563	99.8	837	14	US-10-180-552-352	Sequence 352, App
23	4563	99.8	837	14	US-10-180-557-352	Sequence 352, App
24	4563	99.8	837	14	US-10-173-700-352	Sequence 352, App
25	4563	99.8	837	14	US-10-174-572-352	Sequence 352, App
26	4563	99.8	837	14	US-10-174-579-352	Sequence 352, App
27	4563	99.8	837	14	US-10-174-582-352	Sequence 352, App
28	4563	99.8	837	14	US-10-174-588-352	Sequence 352, App
29	4563	99.8	837	14	US-10-175-739-352	Sequence 352, App
30	4563	99.8	837	14	US-10-175-740-352	Sequence 352, App
31	4563	99.8	837	14	US-10-175-743-352	Sequence 352, App
32	4563	99.8	837	14	US-10-176-488-352	Sequence 352, App
33	4563	99.8	837	14	US-10-176-492-352	Sequence 352, App
34	4563	99.8	837	14	US-10-176-747-352	Sequence 352, App
35	4563	99.8	837	14	US-10-176-750-352	Sequence 352, App
36	4563	99.8	837	14	US-10-176-985-352	Sequence 352, App
37	4563	99.8	837	14	US-10-176-987-352	Sequence 352, App
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40	4563	99.8	837	14	US-10-184-658-352	Sequence 352, App
41	4563	99.8	837	14	US-10-176-991-352	Sequence 352, App
42	4563	99.8	837	14	US-10-173-695-352	Sequence 352, App
43	4563	99.8	837	14	US-10-173-697-352	Sequence 352, App
44	4563	99.8	837	14	US-10-173-705-352	Sequence 352, App
45	4563	99.8	837	14	US-10-174-576-352	Sequence 352, App

ALIGNMENTS

RESULT 1

US-10-247-685-2
; Sequence 2, Application US/10247685
; Publication No. US20030108998A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: AGGREGAN DEGRADING METALLO PROTEASES
; FILE REFERENCE: DM6909D
; CURRENT APPLICATION NUMBER: US/10/247,685
; CURRENT FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 2
; LENGTH: 837
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-247-685-2

Query Match 100.0%; Score 4570; DB 14; Length 837;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 837; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MSQTGSHPGRLAGRWLWGAQPCLLLPVPLSWLWLLLLLLASLLPSARLASPLPREE	60
DB	1	MSQTGSHPGRLAGRWLWGAQPCLLLPVPLSWLWLLLLLLASLLPSARLASPLPREE	60
QY	61	IVFPEKLINGSVLPGSGAPARLLCRQAQFCTLLLELLEODSGVQVEGLTVQYLGQAPELLG	120
DB	61	IVFPEKLINGSVLPGSGAPARLLCRQAQFCTLLLELLEODSGVQVEGLTVQYLGQAPELLG	120
QY	121	GAEPGYLTGTINGDPESVASLHWDCGALLGVLYRGAELHLQPLEGGTTPNSAGGFGAHI	180
DB	121	GAEPGYLTGTINGDPESVASLHWDCGALLGVLYRGAELHLQPLEGGTTPNSAGGFGAHI	180
QY	181	LRKSPASQGGPMCNVKAFLGSPSPRRPRKAPASLSRFVETLVVADDDKMAAFHAGLKKR	240

181 LRRKSPASQGMVNCVKAELGSPSPRRRAKRFASLSRFVETLVVADKMAAFHAGLKR 240
 241 YLLTVMMAAAKAFKHPISIRNPVSLVTRVLVILGSEEGPQVGPSSAAQTILRSCAWORGLN 300
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 361 HELGHVFNMLHDSKPCISLNGPLSTRHVMAVMAHVDPEEPWSPCSARFITDFLDNGY 420
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 421 GHCLLDKPEAPLHLPVTFPGKDYADRCQCLTFGPDSTRHCPQLPPPCAALWCSGHLNGHA 480
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 541 QFSRDCTRPVPRNGGKYCEGRTRFRSCNTEDCPTGSALTFRBEOCAAYNHRTDLFKSF 600
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 661 GCDRIIGSKKKFKDKMVCVCGDGGSCSKQSGFRKFRYGYNNVVTIPAGATHILVROQGNP 720
 721 GHSIYLALKLPDGSYALNGEYTLMPSPDVLPGAVSLRYSGATAASETLSHGGLAQP 780
 721 GHSIYLALKLPDGSYALNGEYTLMPSPDVLPGAVSLRYSGATAASETLSHGGLAQP 780
 781 LTLQVLVAGNPQDTRLRYSFVPRPTPTPTPDQWLHRRRAQILEILRRRPWAGRK 837
 781 LTLQVLVAGNPQDTRLRYSFVPRPTPTPTPDQWLHRRRAQILEILRRRPWAGRK 837

RESULT 2

US-10-408-765A-1348
 ; Sequence 1348, Application US/10408765A
 ; Publication No. US20040101874A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ghosh, Soumitra S.
 ; APPLICANT: Fahy, Eoin D.
 ; APPLICANT: Zhang, Bing
 ; APPLICANT: Gibson, Bradford W.
 ; APPLICANT: Taylor, Steven W.
 ; APPLICANT: Glenn, Gary M.
 ; APPLICANT: Wartock, Dale E.
 ; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
 ; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
 ; FILE REFERENCE: 660088.465
 ; CURRENT APPLICATION NUMBER: US/10/408.765A
 ; CURRENT FILING DATE: 2003-04-04
 ; NUMBER OF SEQ ID NOS: 3077
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1348
 ; LENGTH: 837
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-408-765A-1348

Query Match 100.0%; Score 4570; DB 16; Length 837;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 837; Conservative 0; Mismatches 0; Gaps 0;
 1 MSQTGSHGPRGLAGRWLWGAQPCILLPIVPLSWLWLLLLASLLPSARLASPLPREEE 60

1 MSQTGSHGPRGLAGRWLWGAQPCILLPIVPLSWLWLLLLASLLPSARLASPLPREEE 60
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 61 IVFPEKLVNGSLVPGSGAPARLLCRLOAFGETILLLEQDSGVQVEGLTVQVILGQAPPELLG 120
 121 GAEPGTLYLTGTINGDPESVASLHMDGGALLGVLYRGAEHLQPLEGGTPNSAGPFGAHI 180
 121 GAEPGTLYLTGTINGDPESVASLHMDGGALLGVLYRGAEHLQPLEGGTPNSAGPFGAHI 180
 181 LRRKSPASQGMVNCVKAELGSPSPRRRAKRFASLSRFVETLVVADKMAAFHAGLKR 240
 181 LRRKSPASQGMVNCVKAELGSPSPRRRAKRFASLSRFVETLVVADKMAAFHAGLKR 240
 241 YLLTVMMAAAKAFKHPISIRNPVSLVTRVLVILGSEEGPQVGPSSAAQTILRSCAWORGLN 300
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 361 HELGHVFNMLHDSKPCISLNGPLSTRHVMAVMAHVDPEEPWSPCSARFITDFLDNGY 420
 421 GHCLLDKPEAPLHLPVTFPGKDYADRCQCLTFGPDSTRHCPQLPPPCAALWCSGHLNGHA 480
 421 GHCLLDKPEAPLHLPVTFPGKDYADRCQCLTFGPDSTRHCPQLPPPCAALWCSGHLNGHA 480
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 481 MCOTKHSPPWADGTPCGPAQACMGGRCLHMDQLQDFNIPOAGGWPMPGWDGCSRTCGGV 540
 541 QFSRDCTRPVPRNGGKYCEGRTRFRSCNTEDCPTGSALTFRBEOCAAYNHRTDLFKSF 600
 541 QFSRDCTRPVPRNGGKYCEGRTRFRSCNTEDCPTGSALTFRBEOCAAYNHRTDLFKSF 600
 601 PGMDWVPRTYGTVAPODQCKLTQARALGYVYVLEPRVVDGTPCSPDSSVCVQGRCIHA 660
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 781 LTLQVLVAGNPQDTRLRYSFVPRPTPTPTPDQWLHRRRAQILEILRRRPWAGRK 837
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RESULT 3

US-10-628-432-1
 ; Sequence 1, Application US/10628432
 ; Publication No. US20040142863A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wyeth
 ; TITLE OF INVENTION: Modified ADAMTS4 molecules
 ; FILE REFERENCE: AM101378
 ; CURRENT APPLICATION NUMBER: US/10/628.432
 ; CURRENT FILING DATE: 2003-07-29
 ; NUMBER OF SEQ ID NOS: 53
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1
 ; LENGTH: 837
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-628-432-1

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Query Match      100.0%; Score 4570; DB 16; Length 837;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 837; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSQTGSHPGRLAGRWLWGAQPCLLPIVPLSLVWMLLLLLASLPSARLASPLPREEE 60
DB 1 MSQTGSHPGRLAGRWLWGAQPCLLPIVPLSLVWMLLLLLASLPSARLASPLPREEE 60

QY 61 IVEPEKLSVLPFGSGAPARLLCRLQAFGTELLLEQDSGVQVEGLTVQYLQAPPELLG 120
DB 61 IVEPEKLSVLPFGSGAPARLLCRLQAFGTELLLEQDSGVQVEGLTVQYLQAPPELLG 120

QY 121 GAEPGTLYLTCTINGDPESVASLHWDGGLLVQYRGAEHLHLPLEGSTPNSAGGPGCAHI 180
DB 121 GAEPGTLYLTCTINGDPESVASLHWDGGLLVQYRGAEHLHLPLEGSTPNSAGGPGCAHI 180

QY 181 LRRKSPASGQGPCNWKAPLGSPSPRRPRAKRFASLSRFVETLVVADDKMAAFHAGLKR 240
DB 181 LRRKSPASGQGPCNWKAPLGSPSPRRPRAKRFASLSRFVETLVVADDKMAAFHAGLKR 240

QY 241 YLLTVMAAAKAFKHPISIRNPVSLVTRVLVILGSGEGPQVPSAAQTLSFCAWORGLN 300
DB 241 YLLTVMAAAKAFKHPISIRNPVSLVTRVLVILGSGEGPQVPSAAQTLSFCAWORGLN 300

QY 301 TPEDSDPDHFDTAILFTRODLGCVSTCDTLGMADVGTVCDPARSCAIVEDDGLQSAFTAA 360
DB 301 TPEDSDPDHFDTAILFTRODLGCVSTCDTLGMADVGTVCDPARSCAIVEDDGLQSAFTAA 360

QY 361 HELGHVFNMLHNSKPCISLNGPLSTRHVMAVPMHADVPEEPWSPCSARFITDFLDNGY 420
DB 361 HELGHVFNMLHNSKPCISLNGPLSTRHVMAVPMHADVPEEPWSPCSARFITDFLDNGY 420

QY 421 GHCLLDKPEAPLHLPTVTFPGKYDADRCQCLTFCGDSRHCQPLPPCAALWCSGHLNGHA 480
DB 421 GHCLLDKPEAPLHLPTVTFPGKYDADRCQCLTFCGDSRHCQPLPPCAALWCSGHLNGHA 480

QY 481 MCQTKHSPWADGTPCGPAQACMGRCCLHMDQLQDFNIPOAGGWGPMGWGDCSRTCGGV 540
DB 481 MCQTKHSPWADGTPCGPAQACMGRCCLHMDQLQDFNIPOAGGWGPMGWGDCSRTCGGV 540

QY 541 QFSRDCTRPVPRNGKYCEGRTRFRSCNTEDCPTGSAITFREEOCAAYNHRITDLFKSF 600
DB 541 QFSRDCTRPVPRNGKYCEGRTRFRSCNTEDCPTGSAITFREEOCAAYNHRITDLFKSF 600

QY 601 PGMDWVPRYTGVAPODQCKLTQARALGYVYVLEPRVVDGTPCSPDSSVCVQGRCIHA 660
DB 601 PGMDWVPRYTGVAPODQCKLTQARALGYVYVLEPRVVDGTPCSPDSSVCVQGRCIHA 660

QY 661 GCDRIIGSKKKFKDKCMVCGDGGSGCSKQSGSFRKFRYGYNNVVTIPAGATHILVROQGNP 720
DB 661 GCDRIIGSKKKFKDKCMVCGDGGSGCSKQSGSFRKFRYGYNNVVTIPAGATHILVROQGNP 720

QY 721 GHRISYIALKLPDGSVALNGEYTLMPSPDVLPGAVSLRYSGATAAETLSHGGLAQP 780
DB 721 GHRISYIALKLPDGSVALNGEYTLMPSPDVLPGAVSLRYSGATAAETLSHGGLAQP 780

QY 781 LTLQVLVAGNPQDTRLRYSFVPRPTPTPQDWLHRRRAQILILRRRPWAGRK 837
DB 781 LTLQVLVAGNPQDTRLRYSFVPRPTPTPQDWLHRRRAQILILRRRPWAGRK 837
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RESULT 4

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US-10-628-432-29
; Sequence 29, Application US/10628432
; Publication No. US20040142863A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Modified ADAMTS4 molecules
; FILE REFERENCE: AM101378
; CURRENT APPLICATION NUMBER: US/10/628,432
; CURRENT FILING DATE: 2003-07-29
; NUMBER OF SEQ ID NOS: 53
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 846
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: ADAMTS4 with active-site mutation
; US-10-628-432-29
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Query Match      99.9%; Score 4567; DB 16; Length 846;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 836; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MSQTGSHPGRLAGRWLWGAQPCLLPIVPLSLVWMLLLLLASLPSARLASPLPREEE 60

QY 61 IVEPEKLSVLPFGSGAPARLLCRLQAFGTELLLEQDSGVQVEGLTVQYLQAPPELLG 120
DB 61 IVEPEKLSVLPFGSGAPARLLCRLQAFGTELLLEQDSGVQVEGLTVQYLQAPPELLG 120

QY 121 GAEPGTLYLTCTINGDPESVASLHWDGGLLVQYRGAEHLHLPLEGSTPNSAGGPGCAHI 180
DB 121 GAEPGTLYLTCTINGDPESVASLHWDGGLLVQYRGAEHLHLPLEGSTPNSAGGPGCAHI 180

QY 181 LRRKSPASGQGPCNWKAPLGSPSPRRPRAKRFASLSRFVETLVVADDKMAAFHAGLKR 240
DB 181 LRRKSPASGQGPCNWKAPLGSPSPRRPRAKRFASLSRFVETLVVADDKMAAFHAGLKR 240

QY 241 YLLTVMAAAKAFKHPISIRNPVSLVTRVLVILGSGEGPQVPSAAQTLSFCAWORGLN 300
DB 241 YLLTVMAAAKAFKHPISIRNPVSLVTRVLVILGSGEGPQVPSAAQTLSFCAWORGLN 300

QY 301 TPEDSDPDHFDTAILFTRODLGCVSTCDTLGMADVGTVCDPARSCAIVEDDGLQSAFTAA 360
DB 301 TPEDSDPDHFDTAILFTRODLGCVSTCDTLGMADVGTVCDPARSCAIVEDDGLQSAFTAA 360

QY 361 HELGHVFNMLHNSKPCISLNGPLSTRHVMAVPMHADVPEEPWSPCSARFITDFLDNGY 420
DB 361 HELGHVFNMLHNSKPCISLNGPLSTRHVMAVPMHADVPEEPWSPCSARFITDFLDNGY 420

QY 421 GHCLLDKPEAPLHLPTVTFPGKYDADRCQCLTFCGDSRHCQPLPPCAALWCSGHLNGHA 480
DB 421 GHCLLDKPEAPLHLPTVTFPGKYDADRCQCLTFCGDSRHCQPLPPCAALWCSGHLNGHA 480

QY 481 MCQTKHSPWADGTPCGPAQACMGRCCLHMDQLQDFNIPOAGGWGPMGWGDCSRTCGGV 540
DB 481 MCQTKHSPWADGTPCGPAQACMGRCCLHMDQLQDFNIPOAGGWGPMGWGDCSRTCGGV 540

QY 541 QFSRDCTRPVPRNGKYCEGRTRFRSCNTEDCPTGSAITFREEOCAAYNHRITDLFKSF 600
DB 541 QFSRDCTRPVPRNGKYCEGRTRFRSCNTEDCPTGSAITFREEOCAAYNHRITDLFKSF 600

QY 601 PGMDWVPRYTGVAPODQCKLTQARALGYVYVLEPRVVDGTPCSPDSSVCVQGRCIHA 660
DB 601 PGMDWVPRYTGVAPODQCKLTQARALGYVYVLEPRVVDGTPCSPDSSVCVQGRCIHA 660

QY 661 GCDRIIGSKKKFKDKCMVCGDGGSGCSKQSGSFRKFRYGYNNVVTIPAGATHILVROQGNP 720
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QY 721 GHRISYIALKLPDGSVALNGEYTLMPSPDVLPGAVSLRYSGATAAETLSHGGLAQP 780
DB 721 GHRISYIALKLPDGSVALNGEYTLMPSPDVLPGAVSLRYSGATAAETLSHGGLAQP 780

QY 781 LTLQVLVAGNPQDTRLRYSFVPRPTPTPQDWLHRRRAQILILRRRPWAGRK 837
DB 781 LTLQVLVAGNPQDTRLRYSFVPRPTPTPQDWLHRRRAQILILRRRPWAGRK 837
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RESULT 5

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US-10-358-283-11
; Sequence 11, Application US/10358283
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Publication No. US20040054149A1
GENERAL INFORMATION:
APPLICANT: WYETH
TITLE OF INVENTION: TRUNCATED AGGREGANASE MOLECULES
FILE REFERENCE: 08702-0112-00000
CURRENT APPLICATION NUMBER: US/10/358,283
CURRENT FILING DATE: 2003-02-17
PRIOR APPLICATION NUMBER: 60/354,592
PRIOR FILING DATE: 2002-02-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 11
LENGTH: 837
TYPE: PRT
ORGANISM: Homo sapiens
US-10-358-283-11

Query Match      99.9%; Score 4566; DB 15; Length 837;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 836; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSQTGSHPGRLAGRLMWAQPCLLPIVPLSLWMLLLLLLASLLPSARLASPLPREE 60
DB 1 MSQTGSHPGRLAGRLMWAQPCLLPIVPLSLWMLLLLLLASLLPSARLASPLPREE 60
QY 61 IVPEKLINGSVLPSCGAPALLCRLQAFGETLLELEQDSGVQVVEGLTVOYLQAPPELLG 120
DB 61 IVPEKLINGSVLPSCGAPALLCRLQAFGETLLELEQDSGVQVVEGLTVOYLQAPPELLG 120
QY 121 GAEFGTYLTCTINGDPESVASLHWDGALLGVLYRGAELHLQPLEGGTSPNSAGGPGCAHI 180
DB 121 GAEFGTYLTCTINGDPESVASLHWDGALLGVLYRGAELHLQPLEGGTSPNSAGGPGCAHI 180
QY 181 LRKSPASGGQPCNWKAPLGSPPSPRRRAKRPASLSRFVETLVVADDDKMAAHHGAGLKR 240
DB 181 LRKSPASGGQPCNWKAPLGSPPSPRRRAKRPASLSRFVETLVVADDDKMAAHHGAGLKR 240
QY 241 YLITVMAAAKAFKHSIRNPVSLVTRVLILSGEGPGVGPSSAQTLSFCAWORGSLN 300
DB 241 YLITVMAAAKAFKHSIRNPVSLVTRVLILSGEGPGVGPSSAQTLSFCAWORGSLN 300
QY 301 TPEDSDPDHFDTAILFTRODLGCVSTCDTLGMADVGTVCDPARSCAIVEDDGLQSAFTAA 360
DB 301 TPEDSDPDHFDTAILFTRODLGCVSTCDTLGMADVGTVCDPARSCAIVEDDGLQSAFTAA 360
QY 361 HELGHVFNMLHDNSKPCISLNGPLSTSRHVPAPMAHVDPDEEPPSPCSARFITDFLDNGY 420
DB 361 HELGHVFNMLHDNSKPCISLNGPLSTSRHVPAPMAHVDPDEEPPSPCSARFITDFLDNGY 420
QY 421 GHCLLDKPEAPLHLVPTFPKGDYDADRCQCLTFGPDSDRHCPQLPPPCAAALWCSGHLNGHA 480
DB 421 GHCLLDKPEAPLHLVPTFPKGDYDADRCQCLTFGPDSDRHCPQLPPPCAAALWCSGHLNGHA 480
QY 481 MCQTKHSPWADGTPCGPAQACMGRCLHMDQLQDFNIPQAGGMPGMPGWDGCSRTCCGVV 540
DB 481 MCQTKHSPWADGTPCGPAQACMGRCLHMDQLQDFNIPQAGGMPGMPGWDGCSRTCCGVV 540
QY 541 QFSRSDCTRPVPRNGGKYCEGRTRFRSCNTEDCTGSALTFRFEEQCAAYNHRITDLFKSF 600
DB 541 QFSRSDCTRPVPRNGGKYCEGRTRFRSCNTEDCTGSALTFRFEEQCAAYNHRITDLFKSF 600
QY 601 PGPMDWPRYTGVAPOQCKLTCCARALGYVYVLEPRVWDGTGCPSPDSSSVVCVQGRCIHA 660
DB 601 PGPMDWPRYTGVAPOQCKLTCCARALGYVYVLEPRVWDGTGCPSPDSSSVVCVQGRCIHA 660
QY 661 GCDRIIGSKKFKDKMVCVGGDSCGSCSKQSGFRKFRYGYNNVVTIPAGATHILVRQGNP 720
DB 661 GCDRIIGSKKFKDKMVCVGGDSCGSCSKQSGFRKFRYGYNNVVTIPAGATHILVRQGNP 720
QY 721 GHSIYIALKLPGSYALNGEYTLMPSPDVTDLVPGAVSLRYSGATASETLSHGHPAQP 780
DB 721 GHSIYIALKLPGSYALNGEYTLMPSPDVTDLVPGAVSLRYSGATASETLSHGHPAQP 780

104 QY 781 LTLQVLVAGNPQDTRLRYSFVPRPTPTPDQWLHRRRAQILILEILRRRPWAGSK 837
DB 781 LTLQVLVAGNPQDTRLRYSFVPRPTPTPDQWLHRRRAQILILEILRRRPWAGSK 837

RESULT 6
US-09-946-374-317
Sequence 317, Application US/09946374
Publication No. US20030073129A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Fan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumaas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830P1C1
CURRENT APPLICATION NUMBER: US/09/946,374
CURRENT FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: 60/098716
PRIOR FILING DATE: 1998-09-01
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57 PRIOR APPLICATION NUMBER: 60/105693
58 PRIOR FILING DATE: 1998-10-26
59 PRIOR APPLICATION NUMBER: 60/105694
60 PRIOR FILING DATE: 1998-10-26
61 PRIOR APPLICATION NUMBER: 60/105807

Query Match 99.8%; Score 4563; DB 10; Length 837;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 836; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSQTGSHPCGRGLAGRWLWGAQPCLLPIVPLSLVWLLLLLLASLPASLPREEE 60

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QY 61 IVFPEKINGSVLPFGSGAPARLLCRLOAFGETLLELEQDSGVQVEGLTVQYLQAPELLG 120

Db 61 IVFPEKINGSVLPFGSGAPARLLCRLOAFGETLLELEQDSGVQVEGLTVQYLQAPELLG 120

Fri Apr 1 15:02:40 2005

us-09-634-287e-2.rapb

QY 121 GAEPGYLTGTINGDPESVASLHWDGALLGVLYRGAELHLOPLEGGTSPNSAGPGGAI 180
 Db 121 GAEPGYLTGTINGDPESVASLHWDGALLGVLYRGAELHLOPLEGGTSPNSAGPGGAI 180
 QY 181 LRKSPASOGGPMCNVKAFLGSPSPRRRAKAPASLRSFVETLVVADDDKMAAFHAGLKR 240
 Db 181 LRKSPASOGGPMCNVKAFLGSPSPRRRAKAPASLRSFVETLVVADDDKMAAFHAGLKR 240
 QY 241 YLLTWAAAKAFKPSIRNPVSLVTRVLVILGSGEGPQVGPSPASAAOTLRSFCAMORGLN 300
 Db 241 YLLTWAAAKAFKPSIRNPVSLVTRVLVILGSGEGPQVGPSPASAAOTLRSFCAMORGLN 300
 QY 301 TPEDSPDHDFTAILTRDQCGVSTCDTLGMADVTCVCDPARSCAIVEDDGLQSAFTAA 360
 Db 301 TPEDSPDHDFTAILTRDQCGVSTCDTLGMADVTCVCDPARSCAIVEDDGLQSAFTAA 360
 QY 361 HELGHVFNMLHDSKPCISLNGPLSTRHVMAPVMAHVDPPEWSPCSARFITDPLDNGY 420
 Db 361 HELGHVFNMLHDSKPCISLNGPLSTRHVMAPVMAHVDPPEWSPCSARFITDPLDNGY 420
 QY 421 GHCLLDKPEAPLHLVTFPPCKDYADRCQCOLTFGPDSSRHCPCQLPPPCAALWCSGHLNGHA 480
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 Db 481 MCQTKHSFWDGTPCGPAQACMGRCCLHMDQLODFNIPOAGGWPMPGWDGCSRTCCGGV 540
 QY 541 QFSRDCTRVPRNGKYGCEGRTRESCNTECPTGSALTFRBEOCAAYNHRTDLFKSF 600
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 QY 721 GHSIYLALKPDGSGYALNGEYTLMPSPDVLVPGAVSLRYSGATAASETLSHGHPLAQP 780
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 QY 781 LTLQVLVAGNQDTRLRYSFVFPRTPTPTQDMLHRAQILRLRRPWAGRK 837
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RESULT 7
 US-10-052-586-352
 ; Sequence 352, Application US/10052586
 ; Publication No. US20020127584A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Pan, James
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: ACIDS ENCODING THE SAME
 ; FILE REFERENCE: P3430R1C1
 ; CURRENT APPLICATION NUMBER: US/10/052,586
 ; CURRENT FILING DATE: 2002-01-15
 ; PRIOR APPLICATION NUMBER: 60/059263
 ; PRIOR FILING DATE: 1997-09-18
 ; PRIOR APPLICATION NUMBER: 60/059266
 ; PRIOR FILING DATE: 1997-09-18
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Query Match 99.8%; Score 4563; DB 13; Length 837;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 836; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSQTGSHPGRLAGRLWGAQPCLLPIVPLSWLWLLLLASLLPSARLASPLPREEE 60
Db 1 MSQTGSHPGRLAGRLWGAQPCLLPIVPLSWLWLLLLASLLPSARLASPLPREEE 60
Qy 61 IVFPEKLSVLPFGSGAPARLLCRQAFCETLLELEQDSGVQVEGLTVQYLQAPPELLG 120
Db 61 IVFPEKLSVLPFGSGAPARLLCRQAFCETLLELEQDSGVQVEGLTVQYLQAPPELLG 120
Qy 121 GAEPGTILGTINGDPESVASLHWGALLGVLYRGAELHLQPLEGGTPNSAGGFAHI 180
Db 121 GAEPGTILGTINGDPESVASLHWGALLGVLYRGAELHLQPLEGGTPNSAGGFAHI 180
Qy 181 LRRKSPASQGGPMCNVKAFLGSPSPRRPRAKRFASLSRFVETLVVADDKMAAFHGLKLR 240
Db 181 LRRKSPASQGGPMCNVKAFLGSPSPRRPRAKRFASLSRFVETLVVADDKMAAFHGLKLR 240
Qy 241 YLLTVMMAAAKAFKPSIRNPVSLVTRVLVILGSGEGPQVGPSPAAQTLSFCAWQRLN 300
Db 241 YLLTVMMAAAKAFKPSIRNPVSLVTRVLVILGSGEGPQVGPSPAAQTLSFCAWQRLN 300
Qy 301 TPEDSDPHFDFTAILFTRODLGVSTCDTLGMADVGTVCDPARSCAIVEDDGLQSAFTAA 360
Db 301 TPEDSDPHFDFTAILFTRODLGVSTCDTLGMADVGTVCDPARSCAIVEDDGLQSAFTAA 360
Qy 361 HELGHVFNMLHNSKPCISLNGPLSTSRHVMAFVMAHVDPEPWPSPCSARFIFDLDNGY 420
Db 361 HELGHVFNMLHNSKPCISLNGPLSTSRHVMAFVMAHVDPEPWPSPCSARFIFDLDNGY 420
Qy 421 GHCLLDKPEAPLHLVPTFFPKDYDADRCQLTFFGPDSDRHCPLQPPPCAALWCSGHLNGHA 480
Db 421 GHCLLDKPEAPLHLVPTFFPKDYDADRCQLTFFGPDSDRHCPLQPPPCAALWCSGHLNGHA 480
Qy 481 MCQTKHSPWADGTPCGPAQACMGGRCLHMDQLQDFNIPOAGGWPMPGWDGCSRTCCGGV 540
Db 481 MCQTKHSPWADGTPCGPAQACMGGRCLHMDQLQDFNIPOAGGWPMPGWDGCSRTCCGGV 540

241	Db	YLLVTMAAAAKAFKHPISIRNPVSIWVTVTLVILSGEEGPQVGPAAQTLRFSCAWQRLN	300
301	Qy	TPESDPPHFDTAILFTRODLGCVSTCDTLGMADVGTCDPARSCAIVEDDGLQSAFTAA	360
301	Db	TPESDPPHFDTAILFTRODLGCVSTCDTLGMADVGTCDPARSCAIVEDDGLQSAFTAA	360
361	Qy	HELGHVFNLHDNSKPCISLNGPISTSHVNAPVMAHVDPEPWSPCSARITITFLDNGY	420
361	Db	HELGHVFNLHDNSKPCISLNGPISTSHVNAPVMAHVDPEPWSPCSARITITFLDNGY	420
421	Qy	GHLCLDKPEAPLHLPVTPFGKYDADROCOLTFGPDSDRHCQLPOLPPCAALWCSGHLNGHA	480
421	Db	GHLCLDKPEAPLHLPVTPFGKYDADROCOLTFGPDSDRHCQLPOLPPCAALWCSGHLNGHA	480
481	Qy	MCQTKHSPWADGTPCGPAQAACMGGRCLHMDQLQDNFIPOAGWGWPWGDCSRTC GGCV	540
481	Db	MCQTKHSPWADGTPCGPAQAACMGGRCLHMDQLQDNFIPOAGWGWPWGDCSRTC GGCV	540
541	Qy	QPSRSDCTRPVRNGKGYCEGRTEFRSCNTEDCTGSGALTFRBQCAAYNHRITDLFKSF	600
541	Db	QPSRSDCTRPVRNGKGYCEGRTEFRSCNTEDCTGSGALTFRBQCAAYNHRITDLFKSF	600
601	Qy	PGPMDWVPRTYTGVAPODQCKLTCQARALGYVYVLPVRVVDGTPCPDPSSSVCQGRCIHA	660
601	Db	PGPMDWVPRTYTGVAPODQCKLTCQARALGYVYVLPVRVVDGTPCPDPSSSVCQGRCIHA	660
661	Qy	GCDRIIGSKKFFDKCMVCGDGGSGCKSGSKFRKRYGNNVVVTIPAGATHILVROQGNP	720
661	Db	GCDRIIGSKKFFDKCMVCGDGGSGCKSGSKFRKRYGNNVVVTIPAGATHILVROQGNP	720
721	Qy	GHRISYIALKLDPGSYALNGEYTLMPSPDVLPGAVSLRYSGATAASETLSHGGLAQP	780
721	Db	GHRISYIALKLDPGSYALNGEYTLMPSPDVLPGAVSLRYSGATAASETLSHGGLAQP	780
781	Qy	LTLQVLVAGNPQDTRLRYSEFFVRPTPTPTQDMLHRAQILLEILRRPWPAGRK	837
781	Db	LTLQVLVAGNPQDTRLRYSEFFVRPTPTPTQDMLHRAQILLEILRRPWPAGRK	837

RESULT 9

US-10-176-758-352

; Sequence 352, Application US/10176758

; Publication No. US2003000835A1

GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P3430R1C104

; CURRENT APPLICATION NUMBER: US/10/176,758

; PRIOR FILING DATE: 2002-06-21

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 352

; LENGTH: 837

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-176-758-352

Query Match 99.8%; Score 4563; DB 14; Length 837;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 836; Conservative 0; Mismatches 1; Indels 0; Gaps 0

Qy 1 MSQTGSHPGRGLAGRWLGAQPCLLPIVPLSWLWVLLLLLLLLASLLPSARLASPLPREEE 60

QY	541	QFSSRDCTRPVPRNGKCYCEGRTRFRSNTDCTPGSALTREBQCAAYNHRTDLFKSF	600
Db	541	QFSSRDCTRPVPRNGKCYCEGRTRFRSNTDCTPGSALTREBQCAAYNHRTDLFKSF	600
QY	601	PGMDWVPRTYTVAPDQCKLTCQARALGYYVLEPRVVDGTCPCPDSSVCVQGRCIHA	660
Db	601	PGMDWVPRTYTVAPDQCKLTCQARALGYYVLEPRVVDGTCPCPDSSVCVQGRCIHA	660
QY	661	GCDRIIGSKKFKDKMVCVGGDGGSCQSGSFRKFRYGYNNVVVTIPAGATHILVRQQGNP	720
Db	661	GCDRIIGSKKFKDKMVCVGGDGGSCQSGSFRKFRYGYNNVVVTIPAGATHILVRQQGNP	720
QY	721	GHRSIYLALKLPDGSYALNGEYTLMPSPDVLPGAVSLRYSYGATAASETLSGHGPLAQP	780
Db	721	GHRSIYLALKLPDGSYALNGEYTLMPSPDVLPGAVSLRYSYGATAASETLSGHGPLAQP	780
QY	781	LTLQVLVAGNPQDTRLRYSPFVPRPTPSTPRTPQDWLHRRRAQILRLRRRPWAGRK	837
Db	781	LTLQVLVAGNPQDTRLRYSPFVPRPTPSTPRTPQDWLHRRRAQILRLRRRPWAGRK	837
RESULT 8			
US-10-174-590-352			
; Sequence 352, Application US/10174590			
; Publication No. US20030008352A1			
; GENERAL INFORMATION:			
; APPLICANT: Baker, Kevin P.			
; APPLICANT: Chen, Jian			
; APPLICANT: Deenoyers, Luc			
; APPLICANT: Goddard, Audrey			
; APPLICANT: Godowski, Paul J.			
; APPLICANT: Gurney, Austin L.			
; APPLICANT: Pan, James			
; APPLICANT: Smith, Victoria			
; APPLICANT: Watanabe, Colin K.			
; APPLICANT: Wood, William I.			
; APPLICANT: Zhang, Zemin			
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC			
; TITLE OF INVENTION: ACIDS ENCODING THE SAME			
; FILE REFERENCE: P3430R1C42			
; CURRENT APPLICATION NUMBER: US/10/174,590			
; CURRENT FILING DATE: 2002-06-18			
; Prior application removed - See File Wrapper or Palm			
; NUMBER OF SEQ ID NOS: 612			
; SEQ ID NO 352			
; LENGTH: 837			
; TYPE: PRT			
; ORGANISM: Homo Sapien			
US-10-174-590-352			
Query Match 99.8%; Score 4563; DB 14; Length 837;			
Best Local Similarity 99.9%; Pred. No. 0;			
Matches 836; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
QY	1	MSQTGSHPRGRGLAGWLMGAQPCLLLPVLSWLWMLLLLLASLLPSARLASPLPREEE	60
Db	1	MSQTGSHPRGRGLAGWLMGAQPCLLLPVLSWLWMLLLLLASLLPSARLASPLPREEE	60
QY	61	IVFPEKLNGSVLPGSGAPARLLCRIQAFGETLILLEQDSGVQVEGLTVQVIGQAPPELLG	120
Db	61	IVFPEKLNGSVLPGSGAPARLLCRIQAFGETLILLEQDSGVQVEGLTVQVIGQAPPELLG	120
QY	121	GAEPGTYLTTGTTNGDPESVASHWDDGALLGVLYRGAELHLQPLEGCTPNSAGGPGGAAHI	180
Db	121	GAEPGTYLTTGTTNGDPESVASHWDDGALLGVLYRGAELHLQPLEGCTPNSAGGPGGAAHI	180
QY	181	LRRKSPASQGGPMCNVKAFLGSPSPRRPRAKRFASLSRFVETLVVADDKMAAFHGAGLKR	240
Db	181	LRRKSPASQGGPMCNVKAFLGSPSPRRPRAKRFASLSRFVETLVVADDKMAAFHGAGLKR	240
QY	241	YLLTVMMAAAKAFKIPSTIRNPVSLVTRVLVILGSGEEGQVGPSSAQTILRSCAQORGLN	300

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Db 1 MSQTSHPGRGLAGRWLWGAQPCLLPIVPLSWLWLLLLASLLPSARLASPLPRE 60
Qy 61 IVFPEKLNGSVLPSCGAPARLLCRLOAFGETLLLEQDSGVQVGLTVQYLGQAPELLG 120
Db 61 IVFPEKLNGSVLPSCGAPARLLCRLOAFGETLLLEQDSGVQVGLTVQYLGQAPELLG 120
Qy 121 GAEPCTYLTGTINGDPESVASLHWDGALLGVLYQVGAELHLQPLEGGTPNSAGGPGAH 180
Db 121 GAEPCTYLTGTINGDPESVASLHWDGALLGVLYQVGAELHLQPLEGGTPNSAGGPGAH 180
Qy 181 LRKSPASQOGPMCNVKAFLGSPSPRRRAKRFASLSRFVETLVVADDKMAAFHAGLKR 240
Db 181 LRKSPASQOGPMCNVKAFLGSPSPRRRAKRFASLSRFVETLVVADDKMAAFHAGLKR 240
Qy 241 YLLTWMAAAKAFKPSIRNPVSLVTRVLVILGSGEGPQVGPAAQTLSFCAMORGLN 300
Db 241 YLLTWMAAAKAFKPSIRNPVSLVTRVLVILGSGEGPQVGPAAQTLSFCAMORGLN 300
Qy 301 TPEDSDPHDFTAILFTRODLGCVSTCDTLGMADVTGTCDPARSCAIVEDDGLQSAFTAA 360
Db 301 TPEDSDPHDFTAILFTRODLGCVSTCDTLGMADVTGTCDPARSCAIVEDDGLQSAFTAA 360
Qy 361 HELGHVFNMLHNSKPCISLNGPLSTSRHVMAFVMAHVDPEEPWPCSAARFTTDFLDNGY 420
Db 361 HELGHVFNMLHNSKPCISLNGPLSTSRHVMAFVMAHVDPEEPWPCSAARFTTDFLDNGY 420
Qy 421 GHCLLDKPEAPLHLVTPFGKDYDADRCQLTFGPDSDRHCPLPPCAALWCSGHLNGHA 480
Db 421 GHCLLDKPEAPLHLVTPFGKDYDADRCQLTFGPDSDRHCPLPPCAALWCSGHLNGHA 480
Qy 481 MCQTKHSFWADGTPCGPAQACMGGRCLHMDQLQDFNIPOAGGWPWGMDCSRTCCGGV 540
Db 481 MCQTKHSFWADGTPCGPAQACMGGRCLHMDQLQDFNIPOAGGWPWGMDCSRTCCGGV 540
Qy 541 QFSRDCTRPVPRNGKYCEGRTRFRSCNTEDCTGSAITPREOCAAAYNHTDLFKSF 600
Db 541 QFSRDCTRPVPRNGKYCEGRTRFRSCNTEDCTGSAITPREOCAAAYNHTDLFKSF 600
Qy 601 PGMDWVPRYTGVAPODCKLTCQARALGYVYVLEPRVVDGTPCSPDSSVCQGRCHIA 660
Db 601 PGMDWVPRYTGVAPODCKLTCQARALGYVYVLEPRVVDGTPCSPDSSVCQGRCHIA 660
Qy 661 GCDRIIGSKKFKDKCMVCGDGGSGCSKQSGSFRKFRYGYNNVVTIPAGATHILVRQOQNP 720
Db 661 GCDRIIGSKKFKDKCMVCGDGGSGCSKQSGSFRKFRYGYNNVVTIPAGATHILVRQOQNP 720
Qy 721 GHSIYLAALKLPDGSYALNGEYTLMPSPDVLPGAVSLRYSGATAASETLSGHGPLAQP 780
Db 721 GHSIYLAALKLPDGSYALNGEYTLMPSPDVLPGAVSLRYSGATAASETLSGHGPLAQP 780
Qy 781 LTLQVLVAGNPQDTRLRYSFVPRPTPTPQDMLHRRRAQIILEILRRRWPAGRK 837
Db 781 LTLQVLVAGNPQDTRLRYSFVPRPTPTPQDMLHRRRAQIILEILRRRWPAGRK 837
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RESULT 10

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US-10-175-737-352
; Sequence 352, Application US/10175737
; Publication No. US20030013153A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
```

```
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430RIC50
; CURRENT APPLICATION NUMBER: US/10/175,737
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 352
; LENGTH: 837
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-737-352
```

```
Query Match 99.8%; Score 4563; DB 14; Length 837;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 836; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1 MSQTSHPGRGLAGRWLWGAQPCLLPIVPLSWLWLLLLASLLPSARLASPLPRE 60
Db 1 MSQTSHPGRGLAGRWLWGAQPCLLPIVPLSWLWLLLLASLLPSARLASPLPRE 60
Qy 61 IVFPEKLNGSVLPSCGAPARLLCRLOAFGETLLLEQDSGVQVGLTVQYLGQAPELLG 120
Db 61 IVFPEKLNGSVLPSCGAPARLLCRLOAFGETLLLEQDSGVQVGLTVQYLGQAPELLG 120
Qy 121 GAEPCTYLTGTINGDPESVASLHWDGALLGVLYQVGAELHLQPLEGGTPNSAGGPGAH 180
Db 121 GAEPCTYLTGTINGDPESVASLHWDGALLGVLYQVGAELHLQPLEGGTPNSAGGPGAH 180
Qy 181 LRKSPASQOGPMCNVKAFLGSPSPRRRAKRFASLSRFVETLVVADDKMAAFHAGLKR 240
Db 181 LRKSPASQOGPMCNVKAFLGSPSPRRRAKRFASLSRFVETLVVADDKMAAFHAGLKR 240
Qy 241 YLLTWMAAAKAFKPSIRNPVSLVTRVLVILGSGEGPQVGPAAQTLSFCAMORGLN 300
Db 241 YLLTWMAAAKAFKPSIRNPVSLVTRVLVILGSGEGPQVGPAAQTLSFCAMORGLN 300
Qy 301 TPEDSDPHDFTAILFTRODLGCVSTCDTLGMADVTGTCDPARSCAIVEDDGLQSAFTAA 360
Db 301 TPEDSDPHDFTAILFTRODLGCVSTCDTLGMADVTGTCDPARSCAIVEDDGLQSAFTAA 360
Qy 361 HELGHVFNMLHNSKPCISLNGPLSTSRHVMAFVMAHVDPEEPWPCSAARFTTDFLDNGY 420
Db 361 HELGHVFNMLHNSKPCISLNGPLSTSRHVMAFVMAHVDPEEPWPCSAARFTTDFLDNGY 420
Qy 421 GHCLLDKPEAPLHLVTPFGKDYDADRCQLTFGPDSDRHCPLPPCAALWCSGHLNGHA 480
Db 421 GHCLLDKPEAPLHLVTPFGKDYDADRCQLTFGPDSDRHCPLPPCAALWCSGHLNGHA 480
Qy 481 MCQTKHSFWADGTPCGPAQACMGGRCLHMDQLQDFNIPOAGGWPWGMDCSRTCCGGV 540
Db 481 MCQTKHSFWADGTPCGPAQACMGGRCLHMDQLQDFNIPOAGGWPWGMDCSRTCCGGV 540
Qy 541 QFSRDCTRPVPRNGKYCEGRTRFRSCNTEDCTGSAITPREOCAAAYNHTDLFKSF 600
Db 541 QFSRDCTRPVPRNGKYCEGRTRFRSCNTEDCTGSAITPREOCAAAYNHTDLFKSF 600
Qy 601 PGMDWVPRYTGVAPODCKLTCQARALGYVYVLEPRVVDGTPCSPDSSVCQGRCHIA 660
Db 601 PGMDWVPRYTGVAPODCKLTCQARALGYVYVLEPRVVDGTPCSPDSSVCQGRCHIA 660
Qy 661 GCDRIIGSKKFKDKCMVCGDGGSGCSKQSGSFRKFRYGYNNVVTIPAGATHILVRQOQNP 720
Db 661 GCDRIIGSKKFKDKCMVCGDGGSGCSKQSGSFRKFRYGYNNVVTIPAGATHILVRQOQNP 720
Qy 721 GHSIYLAALKLPDGSYALNGEYTLMPSPDVLPGAVSLRYSGATAASETLSGHGPLAQP 780
Db 721 GHSIYLAALKLPDGSYALNGEYTLMPSPDVLPGAVSLRYSGATAASETLSGHGPLAQP 780
Qy 781 LTLQVLVAGNPQDTRLRYSFVPRPTPTPQDMLHRRRAQIILEILRRRWPAGRK 837
Db 781 LTLQVLVAGNPQDTRLRYSFVPRPTPTPQDMLHRRRAQIILEILRRRWPAGRK 837
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RESULT 11
US-10-174-581-352
; Sequence 352, Application US/10174581
; Publication No. US20030017540A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C41
; CURRENT APPLICATION NUMBER: US/10/174,581
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063564
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063734
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/063870
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066120
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/066466
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/066772
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/069335
; PRIOR FILING DATE: 1997-12-11
; PRIOR APPLICATION NUMBER: 60/069425
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: 60/069870
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/068017
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/078886
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078939
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079664
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079786
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/080107
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080194
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080327
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080333
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/081049
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081070
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081195
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081838
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082568
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082569
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082704
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082797
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/083495
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083496
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083499
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083559
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/084366
; PRIOR FILING DATE: 1998-05-05
; PRIOR APPLICATION NUMBER: 60/084414
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084639
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084640
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084643
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/086023
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/086392
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/086486
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087098
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087208
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759

Query Match 99.8%; Score 4563; DB 14; Length 837;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 836; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSQTGSHPGRLAGRWLGAQPCLLPIVPLSWLWLLLLASLLPSARLASPLPREEE 60
DB 1 MSQTGSHPGRLAGRWLGAQPCLLPIVPLSWLWLLLLASLLPSARLASPLPREEE 60

QY 61 IVFPEKLSVLPSCGAPARLLCRLQAFGETLLLEQDSGVQVEGLTVQYLQAPPELLG 120
DB 61 IVFPEKLSVLPSCGAPARLLCRLQAFGETLLLEQDSGVQVEGLTVQYLQAPPELLG 120

QY 121 GAEPGTTLTGTDPESVASLHWDGGLIQLVYRGAEHLQPLEGGTPNSAGPGCAHI 180
DB 121 GAEPGTTLTGTDPESVASLHWDGGLIQLVYRGAEHLQPLEGGTPNSAGPGCAHI 180

QY 181 LRRKSPASGQGMVNCVAPLSPSPRRRAKRFASLSRFVETLVVADDKMAAFHAGLKR 240
DB 181 LRRKSPASGQGMVNCVAPLSPSPRRRAKRFASLSRFVETLVVADDKMAAFHAGLKR 240

QY 241 YLLTWMAAAKAFKHPISIRNPVSLVTRVLVILSGEEGPOVGPSSAAQTLSFCWAGRLN 300
DB 241 YLLTWMAAAKAFKHPISIRNPVSLVTRVLVILSGEEGPOVGPSSAAQTLSFCWAGRLN 300

QY 301 TPEDSDPDHFDTAILFTRODLGVSTCDTLGMADVGTVCDDPARSCAIVEDDGLQSAFTAA 360
DB 301 TPEDSDPDHFDTAILFTRODLGVSTCDTLGMADVGTVCDDPARSCAIVEDDGLQSAFTAA 360

QY 361 HELGHVFNMLHNSKPCISLNGPLSTRHVMAVMAHVDPPEPSPCSARFITDLDNGY 420
DB 361 HELGHVFNMLHNSKPCISLNGPLSTRHVMAVMAHVDPPEPSPCSARFITDLDNGY 420

QY 421 GHCLLDKPEAPLHLVPTFPKDYDADQCQLTFGPDSTRHCPQLPPPCAAALWCSGHLNGHA 480
DB 421 GHCLLDKPEAPLHLVPTFPKDYDADQCQLTFGPDSTRHCPQLPPPCAAALWCSGHLNGHA 480

QY 481 MCQTKHSWADGTFCGPAQAACWGRCLHMDQLQDFNIPOAGGWGPGWGDSCRTCCGV 540
DB 481 MCQTKHSWADGTFCGPAQAACWGRCLHMDQLQDFNIPOAGGWGPGWGDSCRTCCGV 540

QY 541 QFSRDCRTRPVPRNGGKCEGRTRFRSCNTEDCPTGSALTFRBEOCAAYNHRTDLFKSF 600
DB 541 QFSRDCRTRPVPRNGGKCEGRTRFRSCNTEDCPTGSALTFRBEOCAAYNHRTDLFKSF 600

QY 601 PGMDWVPRYTGVAPODQCKLTCQARALGYVYVLEPRVVDGTPCSPDSSVVCVQGRCIHA 660
DB 601 PGMDWVPRYTGVAPODQCKLTCQARALGYVYVLEPRVVDGTPCSPDSSVVCVQGRCIHA 660

QY 661 GCDRIIGSKKFKDKCMVCGDGGSGCSKQSGFRKFRYGYNNVVTIPAGATHILVROQGNP 720
DB 661 GCDRIIGSKKFKDKCMVCGDGGSGCSKQSGFRKFRYGYNNVVTIPAGATHILVROQGNP 720

QY 721 GHRSIYLALKLPDGSYALNGEYTLMPSPDVLVPGAVSLRYSYGATAASETLSHGHPLAQP 780
DB 721 GHRSIYLALKLPDGSYALNGEYTLMPSPDVLVPGAVSLRYSYGATAASETLSHGHPLAQP 780

QY 781 LTLQVLVAGNPQDTRLSYFFVPRTPSTPRTPPOWLHRRRAQILLEILRRRPWAGRK 837
DB 781 LTLQVLVAGNPQDTRLSYFFVPRTPSTPRTPPOWLHRRRAQILLEILRRRPWAGRK 837

RESULT 13
US-10-176-749-352
; Sequence 352, Application US/10176749
; Publication No. US20030017542A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.

APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C76
; CURRENT APPLICATION NUMBER: US/10/176,749
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 352
; LENGTH: 837
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-749-352

Query Match 99.8%; Score 4563; DB 14; Length 837;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 836; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSQTGSHPGRLAGRWLGAQPCLLPIVPLSWLWLLLLASLLPSARLASPLPREEE 60
DB 1 MSQTGSHPGRLAGRWLGAQPCLLPIVPLSWLWLLLLASLLPSARLASPLPREEE 60

QY 61 IVFPEKLSVLPSCGAPARLLCRLQAFGETLLLEQDSGVQVEGLTVQYLQAPPELLG 120
DB 61 IVFPEKLSVLPSCGAPARLLCRLQAFGETLLLEQDSGVQVEGLTVQYLQAPPELLG 120

QY 121 GAEPGTTLTGTDPESVASLHWDGGLIQLVYRGAEHLQPLEGGTPNSAGPGCAHI 180
DB 121 GAEPGTTLTGTDPESVASLHWDGGLIQLVYRGAEHLQPLEGGTPNSAGPGCAHI 180

QY 181 LRRKSPASGQGMVNCVAPLSPSPRRRAKRFASLSRFVETLVVADDKMAAFHAGLKR 240
DB 181 LRRKSPASGQGMVNCVAPLSPSPRRRAKRFASLSRFVETLVVADDKMAAFHAGLKR 240

QY 241 YLLTWMAAAKAFKHPISIRNPVSLVTRVLVILSGEEGPOVGPSSAAQTLSFCWAGRLN 300
DB 241 YLLTWMAAAKAFKHPISIRNPVSLVTRVLVILSGEEGPOVGPSSAAQTLSFCWAGRLN 300

QY 301 TPEDSDPDHFDTAILFTRODLGVSTCDTLGMADVGTVCDDPARSCAIVEDDGLQSAFTAA 360
DB 301 TPEDSDPDHFDTAILFTRODLGVSTCDTLGMADVGTVCDDPARSCAIVEDDGLQSAFTAA 360

QY 361 HELGHVFNMLHNSKPCISLNGPLSTRHVMAVMAHVDPPEPSPCSARFITDLDNGY 420
DB 361 HELGHVFNMLHNSKPCISLNGPLSTRHVMAVMAHVDPPEPSPCSARFITDLDNGY 420

QY 421 GHCLLDKPEAPLHLVPTFPKDYDADQCQLTFGPDSTRHCPQLPPPCAAALWCSGHLNGHA 480
DB 421 GHCLLDKPEAPLHLVPTFPKDYDADQCQLTFGPDSTRHCPQLPPPCAAALWCSGHLNGHA 480

QY 481 MCQTKHSWADGTFCGPAQAACWGRCLHMDQLQDFNIPOAGGWGPGWGDSCRTCCGV 540
DB 481 MCQTKHSWADGTFCGPAQAACWGRCLHMDQLQDFNIPOAGGWGPGWGDSCRTCCGV 540

QY 541 QFSRDCRTRPVPRNGGKCEGRTRFRSCNTEDCPTGSALTFRBEOCAAYNHRTDLFKSF 600
DB 541 QFSRDCRTRPVPRNGGKCEGRTRFRSCNTEDCPTGSALTFRBEOCAAYNHRTDLFKSF 600

QY 601 PGMDWVPRYTGVAPODQCKLTCQARALGYVYVLEPRVVDGTPCSPDSSVVCVQGRCIHA 660
DB 601 PGMDWVPRYTGVAPODQCKLTCQARALGYVYVLEPRVVDGTPCSPDSSVVCVQGRCIHA 660

QY 661 GCDRIIGSKKFKDKCMVCGDGGSGCSKQSGFRKFRYGYNNVVTIPAGATHILVROQGNP 720
DB 661 GCDRIIGSKKFKDKCMVCGDGGSGCSKQSGFRKFRYGYNNVVTIPAGATHILVROQGNP 720

QY 721 GHRSIYLALKLPDGSYALNGEYTLMPSPDVLVPGAVSLRYSYGATAASETLSHGHPLAQP 780
DB 721 GHRSIYLALKLPDGSYALNGEYTLMPSPDVLVPGAVSLRYSYGATAASETLSHGHPLAQP 780

```
QY 781 LTLQVLVAGNPQDTRLRYSFVPRPTPTPDWLHRRRAQILRLRRRPMWGRK 837
|
|
|
Db 781 LTLQVLVAGNPQDTRLRYSFVPRPTPTPDWLHRRRAQILRLRRRPMWGRK 837
|
|
|
RESULT 14
US-10-176-914-352
; Sequence 352, Application US/10176914
; Publication No. US20030017543A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P34301C83
; CURRENT APPLICATION NUMBER: US/10/176,914
; CURRENT FILING DATE: 2002-06-20
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 352
; LENGTH: 837
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-914-352

Query Match 99.8%; Score 4563; DB 14; Length 837;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 836; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSQTGSHPCRGAGRWLWGAQPCLLPIVPLSWLWMLLLLLASLLPSARLASPLPREE 60
Db 1 MSQTGSHPCRGAGRWLWGAQPCLLPIVPLSWLWMLLLLLASLLPSARLASPLPREE 60

QY 61 IVFPEKLINGSVLPGSGAPARLLCRLOAFGETLLELEQDSGVQVEGLTVQYLQAPPELLG 120
Db 61 IVFPEKLINGSVLPGSGAPARLLCRLOAFGETLLELEQDSGVQVEGLTVQYLQAPPELLG 120

QY 121 GAEPGTLYLTGTINGDPESVASLHWDGALLGVLYRGAEHLHQLPLEGGTPNSAGGPGAH 180
Db 121 GAEPGTLYLTGTINGDPESVASLHWDGALLGVLYRGAEHLHQLPLEGGTPNSAGGPGAH 180

QY 181 LRKSPASQGGPMCNVKAPLGSPSPRRPRAKFPASLSRFVETLVVADDKMAAFHAGLAKR 240
Db 181 LRKSPASQGGPMCNVKAPLGSPSPRRPRAKFPASLSRFVETLVVADDKMAAFHAGLAKR 240

QY 241 YLLTMAAAKAFKHPISIRNPVSLVTRVLILGSBEGPQVGPSSAAQTLSRFCAMORGLN 300
Db 241 YLLTMAAAKAFKHPISIRNPVSLVTRVLILGSBEGPQVGPSSAAQTLSRFCAMORGLN 300

QY 301 TPEDSDPDHFDTAILPTRDQLCGVSTCDTLGNADVGTCDPARSCAIVEDDGLQSAFTAA 360
Db 301 TPEDSDPDHFDTAILPTRDQLCGVSTCDTLGNADVGTCDPARSCAIVEDDGLQSAFTAA 360

QY 361 HELGHVFNMLHNSKPCISLNGPLSTRHVMAVPMVAHVDPESPWSCSARFITDFLDNGY 420
Db 361 HELGHVFNMLHNSKPCISLNGPLSTRHVMAVPMVAHVDPESPWSCSARFITDFLDNGY 420

QY 421 GHCLLDKPEAPLHLPTFFPGKYDADRQCQLTFGPDSSRHCPOLPPPCAAALWCSHGLNHA 480
Db 421 GHCLLDKPEAPLHLPTFFPGKYDADRQCQLTFGPDSSRHCPOLPPPCAAALWCSHGLNHA 480

QY 481 MCQTKHSPPWADGTPCGPAQACMGGRCLHMDQLQDFNIPOAGGMPGMPGDCSRTCCGGV 540
|
|
|
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Db 481 MCQTKHSPPWADGTPCGPAQACMGGRCLHMDQLQDFNIPOAGGMPGMPGDCSRTCCGGV 540
QY 541 QFSRSDCTRPVPRNGKCYCEGRRTRFRSCNTDCTGTSALTREEOCAAYNHRITDLFKSF 600
Db 541 QFSRSDCTRPVPRNGKCYCEGRRTRFRSCNTDCTGTSALTREEOCAAYNHRITDLFKSF 600
QY 601 PGPMDWVPRYTGVAPODQCKLTQARALGYVYVLEPRVVDGTPCSPDSSSVCVQGRCIHA 660
Db 601 PGPMDWVPRYTGVAPODQCKLTQARALGYVYVLEPRVVDGTPCSPDSSSVCVQGRCIHA 660
QY 661 GCDRIIGSKKPEDKCMVCGDGGSGSKSGSRKFRYGYNNVVTIPAGATHILVROQGNP 720
Db 661 GCDRIIGSKKPEDKCMVCGDGGSGSKSGSRKFRYGYNNVVTIPAGATHILVROQGNP 720
QY 721 GHRISYLAALKPDGYSVALNGEYTLMPSPDVLPGAVSLRYSGATAASETLSHGHLAQP 780
Db 721 GHRISYLAALKPDGYSVALNGEYTLMPSPDVLPGAVSLRYSGATAASETLSHGHLAQP 780
QY 781 LTLQVLVAGNPQDTRLRYSFVPRPTPTPDWLHRRRAQILRLRRRPMWGRK 837
Db 781 LTLQVLVAGNPQDTRLRYSFVPRPTPTPDWLHRRRAQILRLRRRPMWGRK 837

RESULT 15
US-10-176-915-352
; Sequence 352, Application US/10176915
; Publication No. US20030017544A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P34301C110
; CURRENT APPLICATION NUMBER: US/10/176,915
; CURRENT FILING DATE: 2002-06-21
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 352
; LENGTH: 837
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-915-352

Query Match 99.8%; Score 4563; DB 14; Length 837;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 836; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSQTGSHPCRGAGRWLWGAQPCLLPIVPLSWLWMLLLLLASLLPSARLASPLPREE 60
Db 1 MSQTGSHPCRGAGRWLWGAQPCLLPIVPLSWLWMLLLLLASLLPSARLASPLPREE 60

QY 61 IVFPEKLINGSVLPGSGAPARLLCRLOAFGETLLELEQDSGVQVEGLTVQYLQAPPELLG 120
Db 61 IVFPEKLINGSVLPGSGAPARLLCRLOAFGETLLELEQDSGVQVEGLTVQYLQAPPELLG 120

QY 121 GAEPGTLYLTGTINGDPESVASLHWDGALLGVLYRGAEHLHQLPLEGGTPNSAGGPGAH 180
Db 121 GAEPGTLYLTGTINGDPESVASLHWDGALLGVLYRGAEHLHQLPLEGGTPNSAGGPGAH 180

QY 181 LRKSPASQGGPMCNVKAPLGSPSPRRPRAKFPASLSRFVETLVVADDKMAAFHAGLAKR 240
Db 181 LRKSPASQGGPMCNVKAPLGSPSPRRPRAKFPASLSRFVETLVVADDKMAAFHAGLAKR 240

QY 241 YLLTMAAAKAFKHPISIRNPVSLVTRVLILGSBEGPQVGPSSAAQTLSRFCAMORGLN 300
|
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|
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Db	241	YLLTVMAAAKAFKPSIRNPVSLVVTRVLVILSGSEEGPQVGPFAAQTLRSFCWORG	300
Qy	301	TPEDSDPHDFTAILFTRODLGCVSTCDTLGMADVGTCDPARSCAIVEDDGLQSAFTAA	360
Db	301	TPEDSGDHDFTAILFTRODLGCVSTCDTLGMADVGTCDPARSCAIVEDDGLQSAFTAA	360
Qy	361	HELGHVFNMLHDSKPCISLNGPLSTSRHVMAVPMVAHVDPPEFPWSPCSARFITDFLDNGY	420
Db	361	HELGHVFNMLHDSKPCISLNGPLSTSRHVMAVPMVAHVDPPEFPWSPCSARFITDFLDNGY	420
Qy	421	GHCLLDKPEAPLHLPVTFPGKYDADROCOLTFGPDSDRHCPOLPPECAALWCSGHLNGHA	480
Db	421	GHCLLDKPEAPLHLPVTFPGKYDADROCOLTFGPDSDRHCPOLPPECAALWCSGHLNGHA	480
Qy	481	MCOTKHSFWADGTPCGPAQACMGRCCLHMDQLQDFNIPOAGGWGMPWGDGCSRTCGGV	540
Db	481	MCOTKHSFWADGTPCGPAQACMGRCCLHMDQLQDFNIPOAGGWGMPWGDGCSRTCGGV	540
Qy	541	QFSSRDCTRPVPRNGGKYCEGRTRFRSCNTEDCPTGSALTFRBOCAAYNHRTDLFKSF	600
Db	541	QFSSRDCTRPVPRNGGKYCEGRTRFRSCNTEDCPTGSALTFRBOCAAYNHRTDLFKSF	600
Qy	601	PGMDWVPRTGYAPDOCKLTQOARALGYVYVLEPRVVDGTPCSPDSSVCQGRCIHA	660
Db	601	PGMDWVPRTGYAPDOCKLTQOARALGYVYVLEPRVVDGTPCSPDSSVCQGRCIHA	660
Qy	661	GCDRIIGSKKKFKDKMVCGGDGGSGSKSGSFRKFRYGYNVVTIPAGATHILVRQGNP	720
Db	661	GCDRIIGSKKKFKDKMVCGGDGGSGSKSGSFRKFRYGYNVVTIPAGATHILVRQGNP	720
Qy	721	GHRSIYLALXLPDGSYALNGEYTLMPSPDVLPGAVSLRYSGATAASETLSCGHGPLAOP	780
Db	721	GHRSIYLALXLPDGSYALNGEYTLMPSPDVLPGAVSLRYSGATAASETLSCGHGPLAOP	780
Qy	781	LTLOVLVAGNPQDRLRYSPFVRPPTSTPRTPQDMLHRRRAQILEILRRRPWAGRK	837
Db	781	LTLOVLVAGNPQDRLRYSPFVRPPTSTPRTPQDMLHRRRAQILEILRRRPWAGRK	837

Search completed: April 1, 2005, 12:45:18
Job time : 153 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 12:42:07 ; Search time 51 Seconds
(without alignments)
1579.087 Million cell updates/sec

Title: US-09-634-287E-2
Perfect score: 4570
Sequence: 1 MSQTSHPGRGLAGRWLWGA.....LHRRQAQILEILRRPFWAGRK 837
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4566	99.9	837	2 T00355	hypothetical prote
2	2158	47.2	951	2 T00017	gene ADAMTS-1 prot
3	1375.5	30.1	550	2 T47158	hypothetical prote
4	1317	28.8	1265	2 T21371	hypothetical prote
5	950.5	20.8	1205	2 T18517	procollagen N-endo
6	480.5	10.5	1558	2 C89114	protein C37C3.6a (
7	480.5	10.5	2167	2 T34395	hypothetical prote
8	415.5	9.1	1444	2 T18856	angiogenesis inhib
9	389	8.5	860	2 T18892	hypothetical prote
10	365	8.0	951	2 T00260	hypothetical prote
11	313	6.8	903	2 S60257	meltrin alpha - mo
12	284.5	6.2	957	2 T15976	hypothetical prote
13	268.5	5.9	609	2 S55270	catrocollastatin p
14	268.5	5.9	814	2 G02390	disintegrin-like m
15	267	5.8	616	2 A55796	ecarin precursor -
16	266.5	5.8	1170	1 TSHUP1	thrombospondin 1 p
17	263.5	5.8	1059	2 T22545	hypothetical prote
18	263	5.8	1170	2 A40558	thrombospondin 1 p
19	260	5.7	571	2 S24789	jararhagin C precu
20	253	5.5	480	1 A30065	trigraimin precursor
21	231	5.5	1178	1 A39804	thrombospondin pre
22	250	5.5	419	2 S41607	atrolysin A (EC 3.
23	243	5.3	478	2 A43296	atrolysin E (EC 3.
24	241.5	5.3	610	2 JC7530	vascular apoptosis
25	239.5	5.2	407	2 S66260	metalloproteinase
26	239.5	5.2	549	2 S48169	metalloproteinase
27	237.5	5.2	826	2 A60385	monocyte surface a
28	237.5	5.2	1172	1 TSHUP2	thrombospondin 2 p
29	235.5	5.2	478	2 JC4880	fibrinolytic metal

30	234.5	5.1	617	2 S48160	metalloproteinase
31	233.5	5.1	469	1 S29126	properdin precursor
32	231	5.1	478	2 JQ1301	hemorrhagic protei
33	229	5.0	655	2 JC7850	disintegrin and me
34	228.5	5.0	1172	2 A42587	thrombospondin 2 p
35	227.5	5.0	429	2 A42972	coagulation factor
36	227.5	5.0	481	2 JC4342	fibrinolytic prote
37	225.5	4.9	481	2 S43125	trimucin precursor
38	225	4.9	508	2 T22836	hypothetical prote
39	223.5	4.9	610	2 JC8056	halyasease - Gloydiu
40	221.5	4.8	952	2 T18900	disintegrin and me
41	217.5	4.8	414	1 HYRSAC	atrolysin C (EC 3.
42	217.5	4.8	1074	2 JCS928	semaphorin F precu
43	216.5	4.7	1042	2 T26644	hypothetical prote
44	214.5	4.7	411	1 HYSNFA	fibrolase (EC 3.4.
45	213.5	4.7	414	2 S41609	atrolysin C (EC 3.

ALIGNMENTS

RESULT 1

T00355
hypothetical protein KIAA0688 - human
C:Species: Homo sapiens (man)
C:Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004
C:Accession: T00355
R:Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.,
DNA Res. 5, 169-176, 1998
A:Title: Prediction of the coding sequences of unidentified human genes. X. The complete
A:Reference number: Z14142; MUID:98403880; PMID:9734811
A:Accession: T00355
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-837 <ISH>
A:Cross-references: UNIPROT:O75173; EMBL:AB014588; NID:93327189; PIDN:BAA31663.1; PID:93;
A:Experimental source: brain
C:Genetics:
A:Gene: KIAA0688
P:519-575/Domain: thrombospondin type 1 repeat homology <THR3>

Query Match	99.9%;	Score	4566;	DB	2;	Length	837;
Best Local Similarity	99.9%;	Pred. No.	1.8e-302;				
Matches	836;	Conservative	0;	Mismatches	1;	Indels	0;
Gaps	0;						
Qy	1	MSQTSHPGRGLAGRWLWGAQPCLLPIVPLSWLWLLLLASLLPSARLASPLREE	60				
Db	1	MSQTSHPGRGLAGRWLWGAQPCLLPIVPLSWLWLLLLASLLPSARLASPLREE	60				
Qy	61	IVFPEKLNGSVLPQSGAPARLLCRQAQFETLLLEQDSGVQVEGLTVQYLQAPPELLG	120				
Db	61	IVFPEKLNGSVLPQSGAPARLLCRQAQFETLLLEQDSGVQVEGLTVQYLQAPPELLG	120				
Qy	121	GAEPGTTLTGTTNGDPESVASLHWDGALLGVQVRAELHLQPLEGGTPNSAGGPAHI	180				
Db	121	GAEPGTTLTGTTNGDPESVASLHWDGALLGVQVRAELHLQPLEGGTPNSAGGPAHI	180				
Qy	181	LRKPSAQSGQPMCNVKAPLGSPSPRRRAKFAISREVTLVVADDDKMAFHGAGLKR	240				
Db	181	LRKPSAQSGQPMCNVKAPLGSPSPRRRAKFAISREVTLVVADDDKMAFHGAGLKR	240				
Qy	241	YLLTWMAAAKAFKHPISRNPNVSLVTRLVILGSGEGPQVGPSPAAQTLSFCAMQRLN	300				
Db	241	YLLTWMAAAKAFKHPISRNPNVSLVTRLVILGSGEGPQVGPSPAAQTLSFCAMQRLN	300				
Qy	301	TPEDSDPHDFTAILFTTRQDLGCVSTCDTLGMADVTGTCDPARSCAIVEDDGLQSAFTAA	360				
Db	301	TPEDSDPHDFTAILFTTRQDLGCVSTCDTLGMADVTGTCDPARSCAIVEDDGLQSAFTAA	360				
Qy	361	HELGHVFNMLHDNSKPCISLNGPLSTSRHVMAVMAHVDPEPSPCSARFTDFLDNGY	420				
Db	361	HELGHVFNMLHDNSKPCISLNGPLSTSRHVMAVMAHVDPEPSPCSARFTDFLDNGY	420				

379	Qy	379	SLNGPLS-----TSRHVMAVMAHVDPEEPWSPCSARPIITDFLNGYG- 421
			: : : :
441	Db	441	STYMPVNVCKFQSTKFDKTOFONNEHIMATPLEYNTHPWSPWSPCSAGMLERFLENNRQO 500
			: : : :
422	Qy	422	-HCLLDKPEAPLHLPVTF---PGKDYDADROCOLTFGPDSSRHCPOLPDPCCAAALWCSGHL 476
			: : : :
501	Db	501	TQCLFDPQVERRYEDVFRDEPKKYDAHQCKFVFGPAEELCPYM-PTCRLWLCAATFY 559
			: : : :
477	Qy	477	NGHAMCOKHSIPWADGTPCGPAQA--CMGGRCLHMDQLQDFNIPOA-----GGWGPGWPW 529
			: : : :
560	Db	560	GSQMGCRTOHPMWADGTPCDBSRSMFCHHGACVRL-----APESLTKIDQWGDWRSW 612
			: : : :
530	Qy	530	GDCSRTCGGGVQFSRRDCTRPVPRNGGKYCSGRTRFPSCNTEDCPTGSALTFRBEOCAA 589
			: : : :
613	Db	613	GECSRTC GGGVQKGLRDCDSPKPRNGGKYCVGOREYRSCNTEQCPWDTQ-PYREVQCSB 671
			: : : :
590	Qy	590	YNHRTDLFKSFFGP-MDWVPRYTGTVAPOQCKLTCQARALGVYVYLVPRVVDGTPCSPDS 648
			: : : :
672	Db	672	FNNKDIGIQGVASTNTHWVPKYANVAPNERCKLYCRLSGSAFYLLRDKVDGTPCDRNG 731
			: : : :
649	Qy	649	SSVCVQGRCTHAGCDRIIGSKKKFKDKMVCGGDGGCSKQSGSF-RKFRYGYNNVVTIIPA 707
			: : : :
732	Db	732	DDICVACAMPAGCDHQLHSLTRDKCGVCGGDDSSCKVWGTFTNEQGTFGYNEVMKIPA 791
			: : : :
708	Qy	708	GATHILVRQOQ--NPGHRSIYLALKLPDGSVALNGEYTLMPSPDTDWLPGAVSLRYSRGAT 765
			: : : :
792	Db	792	GSANIDIRQGYNNKEDDNYLSLRANGEFLLNGHFQVSLARQOIAQDVTV-LEISGSD 850
			: : : :
766	Qy	766	AASSTLSGHGFLAQPLTLQVL-VAGNPQDTRLRY 798
			: : : :
851	Db	851	AITERINGTGPIRSDIYVHVLSVSGHPDDISVEY 884
			: : : :

30

Db	732	DDICVAGACMPAGCDHQHSTLRDRDKCGVCGGDSSCKVVGKTFNEQGTGGVNEVWKIPA	791
Qy	708	GATHILVRQQG--NPGHRSYI LALKLPDGSYALNGEYTLMPSPDVLVLPFGAVSLRYS	765
Db	792	GSANIDIRQGYNNKMKEDDNYLSLRANGEFLLNGHFQVLSLARQQAQDTV-LEISGSD	850
Qy	766	AASETLSGHGFLAQLPLTLQVL-VAGNPQDTRLRY	798
Db	851	ALTERINGTPIRSDIYVHVLSVGSHPDISVEY	884

RESULT 5

Tl8517

procollagen N-endopeptidase (EC 3.4.24.14) I - bovine

N;Alternate names: procollagen N-proteinase

C;Species: Bos primigenius taurus (cattle)

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: Tl8517

R;Colige, A.; Nuegens, B.V.; Lapiere, C.M.

submitted to the EMBL Data Library, February 1996

A;Description: Cloning of the cDNA of the bovine procollagen I N-proteinase.

A;Reference number: Zl8941

A;Accession: Tl8517

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-1205 <COL>

RESULT 5

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T18517
procollagen N-endorpeptidase (EC 3.4.24.14) I - bovine
N/Alternate names: procollagen N-proteinase
C/Species: Bos primigenius taurus (cattle)
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T18517
R/Colige, A.; Nusgens, B.V.; Lapiere, C.M.
submitted to the EMBL Data Library, February 1996
A/Description: Cloning of the cDNA of the bovine procollagen I N-proteinase.
A/Reference number: Z18941
A/Accession: T18517
A/Status: preliminary; translated from GB/EMBL/DBBJ
A/Molecule type: mRNA
A/Residues: 1-1205 <COL>
A/Cross-references: UNIPROT:P79331, EMBL:X96389; NID:e990769; PID:e228215; PID:
A/Experimental source: skin
C/Genetics:
A/Gene: PC I-NP
C/Function:
A/Description: catalyzes cleavage of the propeptides of type I and II collagen
C/Keywords: hydrolase; metalloproteinase

Query Match          20.8%; Score 950.5; DB 2; Length 1205;
Best Local Similarity 31.8%; Pred. No. 1.6e-56;
Matches 282; Conservative 119; Mismatches 334; Indels 153; Gaps 42

Qy      8  PGRLAGRWLWGAQPCILLPIVPLSLWLVLLLLLLASLLPSARLASPLP-----R 57
Db      3  PPGAAGR-----LLCPA-----LLLLLLPLPADARLAAAADPPGPGQGHGA 46

Qy      58  EBEIVFP-----EKLNGSVLPGSGAPA-----RLLCLRQ 86
Db      47  ERILAVPVRTDAQRLVSHVVSAATAAGVTRRAAPAIPLSGGSSEDPGGRLFYNYVT 106

Qy      87  AFGETLLLEQDSGVQVEGLTVYQLGQAPLLGGA---EP--GTYL--TGTING--DPES 138
Db      107  VFGRDLHLRLRPNARLVAPGATVWEQGES-----GATRVPEPLLGTCLVGDVAGLAESS 161

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Query Match 20.8%: Score 950.5: DB 2: Length 1205:

Best Local Similarity 31.8%; Pred. No. 1.6e-56;

Matches 282; Conservative 119; Mismatches 334; Indels 153; Gaps 42

[illegible]

QY 8 FGRGLAGRWLDWGAQFCUUEPIVFDLSWLWUUEUUSASUUSPSAKLASDFE-----R 37

Db 3 PPAGAAGR-----LLCPA-----LLLLLLPLPADARLAAAAADPPGGPQGHGA 46

Qy 58 EEEIVFP-----EKLNGSVLPGSGAPA-----RLLCRLQ 86

47 EPTI.AVPVPTDAOGRI.VSHVVSAAATAPAGVPTPRAAPANTPGI.SGSGSEEDPGRI.FYNVT 106

[illegible]

QY 87 AFGETLLELEQDSGVQVEGLTVQYLGQAPELLGA---EP--GTYL-TGTING--DPES 138

[illegible]

Db 107 VFGRDLHLRLRPNARLVAPGATVWQGES-----GATRVEPLLGTCLYVGDVAGLAESS 161

139 VAST:HWDDGGALTGVTQYRGAELHLOPI.EGGTPNSAGGPG-AHTLRKSPASGGGPMCNVK 197

THE UNIVERSITY OF CHICAGO

Qy	519	QAGGPGWPGWDCSRTCGGVOFSSRDCTRPVPRNGGKVCGRTRFRSCNTDCTPGS	578
Db	75	ETGNGWGPWPEVENCSSRCGGVQLEKRCQSGD-----CTGASVRYISCNLNACESGT	126
Qy	579	ALTFREEOCAAYNHRITDLFKSFPFPM-----WVPRYTGVAPQDQCKLTQARALGYVYV	633
Db	127	--DFRAEQCKFNDIA-----LDGNYHKWTP-YKG---KNKCELVCKPESGNFYK	171
Qy	634	LEPRVVDGTPCSPDSSVQVQRCIIHAGCDRIIGSKKPKCMVCGDGGSCSKQSGSF-	692
Db	172	WADKVVDTKCDKSKNDICVDGCLPVGCDGKGLSSLKFDKCKGCDGDSCTKTIERFD	231
Qy	693	-RKFRYGVNNVVTIPAGATHILVRQGNPGHRSIYALKLDPGYSYALNGEYITLMPSTDV	751
Db	232	ERNLSPGVDHDIILPEGATNIKIOEARKSTNN---LALKNGSDHFLYNGN-GLIQVEKV	287
Qy	752	VLPGAVSLRYSGATASETLSHGHPLAQPLTLQVLVAGNPQDTRLRYSFVFP	803
Db	288	EVGGTI---FVYDDAEPETLSAQGLSELTALLFRKGRSDTAIKYFERSIP	336
RESULT 7			
T34395			
hypoetical protein C37C3.6b - Caenorhabditis elegans			
C:Species: Caenorhabditis elegans			
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004			
C:Accession: T34395; T34394			
R:Geisel, C.; Bradshaw, H.			
A:Description: The sequence of C. elegans cosmid C37C3.			
A:Reference number: Z21518			
A:Accession: T34395			
A:Status: preliminary; translated from GB/EMBL/DBJ			
A:Molecule type: DNA			
A:Residues: 1-2167 <GEI>			
A:Cross-references: UNIPROT:076840; EMBL:U64857; PIDN:AAC25868.1; GSPDB:GN00023; CESP:C37C3			
A:Experimental source: strain Bristol N2; clone C37C3			
A:Accession: T34394			
A:Status: preliminary; translated from GB/EMBL/DBJ			
A:Molecule type: DNA			
A:Residues: 1-1555, 'SKF' <GE2>			
A:Cross-references: EMBL:U64857; PIDN:AAC25867.1; GSPDB:GN00023; CESP:C37C3.6a			
A:Experimental source: strain Bristol N2; clone C37C3			
C:Genetics:			
A:Gene: CESP:C37C3.6b; CESP:C37C3.6a			
A:Map position: 5			
A:Introns: 32/3; 104/2; 156/2; 207/1; 459/2; 536/3; 577/2; 1105/3; 1367/1; 1438/1; 1556/1			
Query Match 10.5%; Score 480.5; DB 2; Length 2167;			
Best Local Similarity 35.6%; Pred. No. 2.7e-24; Indels 37; Gaps 10;			
Matches 104; Conservative 46; Mismatches 105;			
Qy	519	QAGGPGWPGWDCSRTCGGVOFSSRDCTRPVPRNGGKVCGRTRFRSCNTDCTPGS	578
Db	75	ETGNGWGPWPEVENCSSRCGGVQLEKRCQSGD-----CTGASVRYISCNLNACESGT	126
Qy	579	ALTFREEOCAAYNHRITDLFKSFPFPM-----WVPRYTGVAPQDQCKLTQARALGYVYV	633
Db	127	--DFRAEQCKFNDIA-----LDGNYHKWTP-YKG---KNKCELVCKPESGNFYK	171
Qy	634	LEPRVVDGTPCSPDSSVQVQRCIIHAGCDRIIGSKKPKCMVCGDGGSCSKQSGSF-	692
Db	172	WADKVVDTKCDKSKNDICVDGCLPVGCDGKGLSSLKFDKCKGCDGDSCTKTIERFD	231
Qy	693	-RKFRYGVNNVVTIPAGATHILVRQGNPGHRSIYALKLDPGYSYALNGEYITLMPSTDV	751
Db	232	ERNLSPGVDHDIILPEGATNIKIOEARKSTNN---LALKNGSDHFLYNGN-GLIQVEKV	287
Qy	752	VLPGAVSLRYSGATASETLSHGHPLAQPLTLQVLVAGNPQDTRLRYSFVFP	803
Db	288	EVGGTI---FVYDDAEPETLSAQGLSELTALLFRKGRSDTAIKYFERSIP	336
Query Match 10.5%; Score 480.5; DB 2; Length 1558;			
Best Local Similarity 35.6%; Pred. No. 1.9e-24; Indels 37; Gaps 10;			
Matches 104; Conservative 46; Mismatches 105;			
Db	162	VALSNCBG--LAGLINMEEREFIEPLEKGLAAKEAQGRVHVHVR-PTTSRPP-----	213
Qy	198	APLGSP-----SPRPRKGFASLSRFVETLVVADDKM	230
Db	214	-PLGGFOALDTGISADSLDSLRALGVLEERVNSRRRRRAADDDYNIIEVLGVDDSV	272
Qy	231	AAFHGA-GLKRYLLTMAAAAFKHPSTRNPSVLVTVTLVILSGEGR--QVGFSAQA	287
Db	273	VQPHGTEHVQKYLTLTLMNIVNEYIHDESGAHNVVLVILLISYKSKSLIEIG-NPSQ	331
Qy	288	TLRSFCAWRGRLTPDSDPDHDTAILFTRLQDLQCVSTCDTLGMADVTGTCDPARSAI	347
Db	332	SLENCWVAYLQKPTDDEYHDHAI FLTRQDF-GPSGMQ--GYAPVTGMCHPVRSCITL	388
Qy	348	VEDDGLQSAFTAHEIGHVFNMLHD-NSKPCISLNGPLSTSRHVAPMAHVDPEEPWSP	406
Db	389	NHEDGFSFAFVAHETGHVLMHEDGQGNRC-----GDEVRLGSIAPLVAQAARHFRHWSR	444
Qy	407	CSARFTIDFLDNGVGHCLLDKP---EAPLHLPTVFPKDYDADRCQLTFGPDSSRHPOL	463
Db	445	CSQQLSRYL-HSY-DCLRDPTFDWPA-LP-QLFGLHYSMNEQCRDFGLGYNMCTAF	500
Qy	464	P--PPCAALWCSHGLNHGAMCQTKHSPADGTPCGPAQACMGRCUHM--DQLODENIQ	519
Db	501	RTFDPCKQLWCS-HPDNPYFCKTKKGPPLDGTMCAPGKHGKFCGHCILWLPDILK----	554
Qy	520	AGHGWPGWDCSRTCGGVOFSSRDCTRPVPRNGGKVCGRTRFRSCNTDCTPGSA	579
Db	555	DGNWGAWSPFSCSRTCGTGVKFRQCDNPNHANGRTCSGLAYDFOLCNSQCDPDLA	614
Qy	580	LTFRFEOCAAYNHRITDL-FKSFPFPMDWVPRYTGVAPQDQCKLTQARALGYVYVLEPRV	638
Db	615	-DFREEQCRW----DLFFEAGQAHHWLPHEHRDA-KERCHLYCESKETGEVVMKRW	668
Qy	639	VDGTPCS-PPSSSVQVQRCIIHAGCDRIIGSKKPKCMVCGDGGSCSKQSGFRKF--	695
Db	669	HDGTRCSYKDAFSLCVRGDCRKGCVGIVSSQEDKCGVCGGNGNSHKVKGITFRSPK	728
Qy	696	RYGVNNVVTIPAGATHILVRQGNPGHRSIYALK-LPDGYSYALNGEYITLMPSTDVLP	754
Db	729	KLGIKWEIPAGARHLLIQEADTTSH--HLAVKNLETGKFLINEENDVDPNSTKPIAM	785
Qy	755	GAVALRYSGATASETLSHGHPLAQPLTLQVLVAGNPQDTRLRYSFVFP	802
Db	786	G-VEVEYRDED-GRETLQTMGLHGTITVVIPEGDAR-ISLTYKIMI	830
RESULT 6			
C89114			
protein C37C3.6a [imported] - Caenorhabditis elegans			
C:Species: Caenorhabditis elegans			
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004			
C:Accession: C89114			
R:Anonymous, The C. elegans Sequencing Consortium.			
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog			
A:Reference number: A75000; PMID:990613; PMID:9851916			
A>Note: see websites genome.wustl.edu/gsc/c_elegans/ and www.sanger.ac.uk/projects/c_ele			
A>Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and			
A:Accession: C89114			
A:Status: preliminary			
A:Molecule type: DNA			
A:Residues: 1-1558 <STO>			
A:Cross-references: UNIPROT:Q81710; GB:chr_V; PIDN:AAC25867.1; PID:G3294501; GSPDB:GN000			
A:Gene: C37C3.6a			
A:Map position: 5			
Query Match 10.5%; Score 480.5; DB 2; Length 1558;			
Best Local Similarity 35.6%; Pred. No. 1.9e-24; Indels 37; Gaps 10;			
Matches 104; Conservative 46; Mismatches 105;			

RESULT 8

T18856
 A:Description: The sequence of C. elegans cosmid T19D2.
 A:Reference number: Z18599
 A:Accession: T18892
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T18856; T24653
 R:McMurray, A.

submitted to the EMBL Data Library, July 1995

A:Reference number: Z19031
 A:Accession: T18856
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1444 <W1>
 A:Cross-references: UNIPROT:Q8MYA9; EMBL:Z50004; PIDN:CAA90293.1; GSPDB:GN00028; CESP:C02B4
 A:Experimental source: clone C02B4
 R:McMurray, A.

submitted to the EMBL Data Library, July 1995

A:Reference number: Z19197
 A:Accession: T24653
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1444 <W12>
 A:Cross-references: EMBL:Z50006; PIDN:CAA90302.1; GSPDB:GN00028; CESP:C02B4.1
 A:Experimental source: clone T07C5
 C:Genetics:
 A:Gene: CESP:C02B4.1
 A:Map position: X
 A:Introns: 25/3; 70/3; 96/3; 139/3; 187/1; 234/2; 282/3; 376/2; 422/2; 478/3; 509/3; 566/3

Query Match 9.1%; Score 415.5; DB 2; Length 1444;
 Best Local Similarity 28.0%; Pred. No. 4.5e-20;
 Matches 134; Conservative 56; Mismatches 161; Indels 127; Gaps 26;

QY	283	PSAAQT-----LRSFCAWQGLNTPED-SPDHFDTAILTRDLCGVSTCDYL	330
DB	282	PSALSTGVHKNQQAQLLDAFCRYQAHMNPGLTDMNHVHGVLITGYDVIHTTT-SVA	340
QY	331	GMADVTCVDPARSCAIVEDDGLQSAFTAAHGLGHVFNMLHD-----NSKPCI--SLNG	382
DB	341	GVAPVARMCDPLFACSLVEGLHLGRSFVLAHENGHNMGVHDGVQNCNKGCCLSAVNG	400
QY	383	PLSTSRHVAPVMAHVDPPEPSPCSARFITDL-----DNGYGHCLLDKPEAPL--HL-	434
DB	401	AGKTT-----WSDCSVREFNAFLQLQDESGRGNCLRDASPLIISTNHL	444
QY	435	PVTFPGKDYADRCQLTFGPDNR-----HCPQLPPPCAALWCSGHLNHGAMCOTKHS	490
DB	445	DLRLPQRTADQCCSYFWGRDYKVEIPNGKAMDDICRILWCG-----NSGSTTSTA	500
QY	491	DGTPCGPAQACMGGRCLHMDQLQDFN---IPQAGGHPWG-----PWGDCSRTCGGVQ	541
DB	501	EGSWCCGANKWKHGQCTHW-----TFGLTPVPIDGSEWGAEGKCPICQCAVSGSITVQ	556
QY	542	FSSRDCTRPVRNGGKYGEGRRTRFRSCNTEDCPTGSALTFRFQ-----CAAYN--HR	593
DB	557	GQHRDCVNPAPNNGGKTCEGANIRGIVCG---ATSSNCLGFTREFFGNKICSSIKYDPHK	613
QY	594	TDLFKSFPGPMWVPRYTGA---PQDQCKLTCQ-----ARALGYYYVLEPRVVDGTPC	644
DB	614	PD-----QQLTGEFHSHTQPCRVWCHLIGSELIRNKGF-----PDGTPC	654
QY	645	SPDSSVVCVQGRCHIHAGCD-----RIIGSK-----KKFDKCMV--CGSDG	682
DB	655	GFD--AYCVGGQCLALSCDKNALVEQPCPRLEGSRVHQWBSWSSECSVSCGLGG	710

RESULT 9

T16892
 A:Description: The sequence of C. elegans cosmid T19D2.
 A:Reference number: Z18599
 A:Accession: T16892
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
 C:Accession: T16892
 R:Bentley, D.

submitted to the EMBL Data Library, July 1995

A:Reference number: Z19031
 A:Accession: T18856
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1444 <W1>
 A:Cross-references: UNIPROT:Q8MYA9; EMBL:Z50004; PIDN:CAA90293.1; GSPDB:GN00028; CESP:C02B4
 A:Experimental source: clone C02B4
 R:McMurray, A.

submitted to the EMBL Data Library, December 1995

A:Description: The sequence of C. elegans cosmid T19D2.
 A:Reference number: Z18599
 A:Accession: T16892
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T18856; T24653
 R:McMurray, A.

submitted to the EMBL Data Library, July 1995

A:Reference number: Z19031
 A:Accession: T18856
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1444 <W1>
 A:Cross-references: UNIPROT:Q22580; EMBL:U42846; MID:g1125809; PID:g1125810; PIDN:AAA8361
 A:Genetics:
 A:Gene: CESP:T19D2.1
 A:Introns: 56/3; 96/1; 171/3; 199/3; 245/2; 293/2; 335/3; 395/3; 426/3; 484/2; 505/3; 561/3

submitted to the EMBL Data Library, July 1995

A:Reference number: Z19197
 A:Accession: T24653
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1444 <W12>
 A:Cross-references: EMBL:Z50006; PIDN:CAA90302.1; GSPDB:GN00028; CESP:C02B4.1
 A:Experimental source: clone T07C5
 C:Genetics:
 A:Gene: CESP:C02B4.1
 A:Map position: X
 A:Introns: 25/3; 70/3; 96/3; 139/3; 187/1; 234/2; 282/3; 376/2; 422/2; 478/3; 509/3; 566/3

Query Match 8.5%; Score 389; DB 2; Length 860;
 Best Local Similarity 24.7%; Pred. No. 1.5e-18;
 Matches 139; Conservative 63; Mismatches 222; Indels 138; Gaps 28;

QY	177	GAHILRRKSPASQGMCMVKAPLSPSPRRKAFASLSRF-----	219
DB	77	GHHVTHKRSIESIDHE-CQFDA---NEDYPEDREIANKMLIRVMVKOIRRAEPHRRDI	132
QY	220	--VETLVVADDKM---AAPHGAGLKYLLTVMAAAK---AFKHPSTRNPNVSLVVTRL	269
DB	133	LTVELAVPADDAWDFKMYGKAAENMHTFIMAVNNIDVLYTORLLQPRINIKIVRY	192
QY	270	VIL-----GSGEQPGVQPSAAQTLLRSFCAWQGLNTPEDSDPHFDTAILFT	317
DB	193	EILKNIPHLNARKHNSGD-----VDRLLDAFCQYQNEINPPNDADPRHWDHALFS	244
QY	318	RQDL---CGVSTCDTLGMADVTCVDPARSCAIVEDDGLQSAFTAAHGLGHVFNMLHDSK	375
DB	245	GYDLHRNGVKT--VAGYAPVKMGCSGVRSCITNEGLDFGSFVVTTHMGHSLGMVHDGDN	302
QY	376	PCISLNGPLTSRHYMAPVMAHVDPPEPSPCSARFITDLDNGYGH-----CLLD	426
DB	303	EC-----DLRCCINSPSVG--SGKTHWSQCSVNMENATFV-----GHLGDDFFPPNCLQD	349
QY	427	KPEAPLHLPVTF-----PGKDYADRCQLTFGPDNR-----CPQLPPPCAALWCSGHLN	477
DB	350	-ASANEQRMVAFKESPPQQLFTLDEQCEIFHGECKHKLKDGQTMQNICQMVWCG--N	405
QY	478	GHAMCQTKHSPWADGTPCGPAQACMGGRCLHMDQLQDFNIPOAGGHPWG--PWGDCSRT	535
DB	406	GEGVIRTAH--PALEGTTCGFMICRQGCQVGSQMLMRVTV--GGWSTWDRP-----APT	457
QY	536	CGG-----GVQFSSRDCTRPVRNGGKYGEGRRTRFRSCNTEDCPTGSALTFR	584
DB	458	CGGRCSQCEIRQIRIMRSIROCNPNPSSNNGAPCGQDEARGMVCHRDVNCNGDSIENYAT	517
QY	585	EQCAAYNHRHTDLFKSPGPMWVPRYTGA---PQDQCKLTC-----QARALGYYYVLE	635
DB	518	RVCSRLRDE---NAIPNTI-----LSGEGMQPEQAMCKIWCLISGSTNIRTVSNF---	564
QY	636	PRVVDGTPCSPSSSVVCVOGRC	657
DB	565	---PDGAPCGP--GQYCIKGEK	581

RESULT 10

T00260
 A:Description: The sequence of C. elegans cosmid T19D2.
 A:Reference number: Z18599
 A:Accession: T00260
 C:Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004
 C:Accession: T00260
 R:Nagase, T.; Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.
 A:Title: Prediction of the coding sequences of unidentified human genes. IX. The complete
 A:Reference number: Z14086; MUID:98290545; PMID:9628581
 A:Accession: T00260
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-951 <NAG>
 A:Cross-references: UNIPROT:O60345; EMBL:AB011177; NID:G3043733; PIDN:BAA25531.1; PID:G3043733
 A:Experimental source: brain

C;Genetics:
A;Note: KIA0605
F;46-106/Domain: thrombospondin type 1 repeat homology <THRI>
Query Match 8.0%; Score 365; DB 2; Length 951;
Best Local Similarity 33.1%; Pred. No. 7.4e-17;
Matches 104; Conservative 32; Mismatches 132; Indels 46; Gaps 16;
QY 523 WGPWGPWDCSRCTCGGVQFSSRDC----TRPVPRNGKGYCEGRRTFRSCNTEDEPTGS 578
DB 50 WGEWTWTAFTSRSCGGVTSQERHCLQORRKSVPGNRTCTGTSKRYQLCRVQECPP-D 108
QY 579 ALTFREBOCAA-----YNHRTDLFKSFPFGPMVPRYTVAPOD-----QCKLTCQAR 626
DB 109 GRSFREBOQCVFNSHVNGRTH-----QWKPPLY-----PDYVHISKPCDLHC-TT 154
QY 627 ALGYVYVLEPRVVDGTPCS--PDSSVCVQRCIHAGCDRIIGSKKFKDKCMVCGDGS GC 685
DB 155 VDGORQLMVP-ARDGTSCKLTDLRGVCSKCEPIGCDGVLFSTHTLDKCGICQGDSSC 213
QY 686 SKSGSFRK--FRYGVNNVVTIPAGATHILVROQGNPHRSIYALKLPDGSVALNGEYT 743
DB 214 THVTGNVRKGNALGVSLVTHIPAGARDIQIVERKKSAD---VLALADEAGYFFNGNYK 270
QY 744 LMPSPDVLVPGAVSLRYSGATASET-----LSHGGLAQPLTLQVL-VAGNPQDTRLRY 798
DB 271 -VDSPKFNFIAGTV-VKYYRRPMVDYETGIEYVVAQGTNOGLNVWVWQNGKSPSITFEY 328
QY 799 SFFVPRPTPTPRP 812
DB 329 TLLQP-PHESRPQP 341
RESULT 11
S60257
meltrin alpha - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C;Accession: S60257
R;Yagami-Hiromasa, T.; Sato, T.; Kurisaki, T.; Kamiyo, K.; Nabeshima, Y.I.; Fujisawa-Seth
Nature 377, 652-656, 1995
A;Title: A metalloprotease-disintegrin participating in myoblast fusion.
A;Reference number: S60257; PMID:7566181
A;Accession: S60257
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-903 <YAG>
A;Cross-references: UNIPROT:Q61824; EMBL:D50411; NID:g1054586; PIDN:BAA08912.1; PID:g105
C;Superfamily: mouse meltrin alpha; disintegrin homology
F;421-503/Domain: disintegrin homology <DIS>
F;1349/Active site: Glu #status predicted
Query Match 6.8%; Score 313; DB 2; Length 903;
Best Local Similarity 22.7%; Pred. No. 2.4e-13;
Matches 214; Conservative 103; Mismatches 393; Indels 234; Gaps 47;
QY 38 LILLIASLLPARLASPLPREIEVFPPEKLSVLT-----PGSGAPAR-----LLCRLQ 86
DB 15 LLLALAGALLAPRAARGMSLDQRAYEVARASLLSKDPGIPGOSIPAKOHDPVLTVOLQ 74
QY 87 AFGETLLLELEQDSGVQVEGLT-VQYL--GQAPPELLGAEFGTYLTGTINGDPESVASLH 143
DB 75 LESRDLIILSLENEGLIANGFTETHYLDGTDVSLTRNHTDHCYVGHVQGDAAASVSL 134
QY 144 WDGGALLVQVYRGAEHLQPLEGGTPNSAGGPGAHILRRKSPASGCGQPMCNVAPLGSP 203
DB 135 -TCSDLRLGLIMPENKTYSLPEMKNNTDSYKLVPAESMTNIOQLCGSQHNKSLNLTMEDVSP 193
QY 204 SPRPRARKEF----ASLSRFVETLVVADDKMAAPFAGL---KRYLLTWMAAAKAFKHP 256
DB 194 GTSQMRARRKHRETUKMTKTYELVIVADNREFQRGKLEKVKQRLIIANHHVDFYR-- 251
QY 257 SIRNPVSLVTVRLVILG-----SGEEGPQVGPSAAQTLSRFCANORGLNTPEDSDPDHPT 312

DB 252 ----PLNI---RIVLVGEVWMDIKCSIQVCPPTFLRHEFLDMRKIKLLPRKS-----HDN 300
QY 313 ALLFTRQDLGVSTCDTLGMADVGVTCDPARSCAIV---EDGQSAFTAHELGHVFN 369
DB 301 AQLISGVYFQGT---TIGMAPIMSMCTAEOAGGVVMDHSDSPGAAVTLAHELGHVFN 356
QY 370 LHDNSKPCISLNGPLSTSRHVWAPVMAHVDPPEPSPCSARFIFDLDNGYGHCLLDKPE 429
DB 357 NHDTLERSCSCBAEAKGCCIMNPSGTGPPF-MVFSSCSRKDLSEASLEKGMCLFNLP 415
QY 430 AFLHLVPVTPGK-----DYDADQOC-----OLTFGPDS-----RHC 460
DB 416 ----VKQAFGRKCGYVEGECDCEPEECTNRCNATTTCLKDPADVCAHGCCBDC 471
QY 461 POLPPPCALWCSHGLNHAMCO-----TKHSP-----WADGTPC-GPAQACMGGR-C-LHM 509
DB 472 -QLRPPGTA--CRGSSNCDLPEFCTGTAPHCPANVYLDHGPCGVGVGYCNGICQTHE 528
QY 510 DLQDFNIPQAGWGPWGPWGDSCRTCGGVQFSSRDCTRPVPRNGKY--C-EGRRTRF 566
DB 529 QQCVTI-----WGP-----GAKPAFGICFERVNSAGDPYNGCKDKSGAF 568
QY 567 RSCNTEDEPTGSALTFRBEEQCAAYNHRDLDLFSKFGPMWVPRYTCVAPQDOCKLTCCQAR 626
DB 569 AKCELRDAKCGKI-----QCQGGASRPVI-----GTNAVSIETNIPQEGGRILCR-- 614
QY 627 ALGYVYVLT-----EP-RVVDGTPCSPDSSVCVQRCIHAGCDRIIGSKKFKDKC-MVCG 679
DB 615 --GTHVYLGDDMPDPGLVLGKCA--EGKICLNRCQNIS---VFG---VHKCAMQCH 663
QY 680 GDGSGCSKQSGSF-----RKFRYGVNNVVTIPAGATHI-LVROQGNPHR---SI 725
DB 664 GRGV-CNNRKNCHCEAHWAPPFCDKFGF-----GSTDSGPVQADNOGLTVGILV 713
QY 726 YIALKLPDGSYALNGEYTL-----PSPTDVLVPGAVSLRYSGATAA 767
DB 714 SILCLLAAGFVYVLRKLTMLRLLFTHKTKTMBKLCVHFSRT-----PSGPHLQAHHTPG 769
QY 768 SETLSHGHL-----AQPLTLQVLVAGNPQDTRLRYSFVP----- 803
DB 770 KGLLMRAHFNTPKDRHSLKQNMDSRPLDARAVPQLQSPQVLLPLHQTTPRAPS 829
QY 804 RPTPSTP-----RPTPDWLHRRRAQILEILRRRP 832
DB 830 RPLPASPFAVRAQAGIRKPSPPQKPLPADPLSRTSLTSALVTRP 873
RESULT 12
T15976
hypothetical protein F08C6.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T15976
R;Bentley, D.
submitted to the EMBL Data Library, June 1995
A;Description: The sequence of C. elegans cosmid F08C6.
A;Reference number: Z18440
A;Accession: T15976
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-957 <BEN>
A;Cross-references: UNIPROT:Q19204; EMBL:U29378; NID:g868184; PID:g868185; PIDN:AAA68721
A;Experimental source: strain Bristol N2
A;Gene: CESP:F08C6.1
A;Introns: 23/1; 135/3; 220/3; 285/3; 325/2; 376/3; 461/2; 498/3; 532/3; 627/2; 714/1; 714/1;
Query Match 6.2%; Score 284.5; DB 2; Length 957;
Best Local Similarity 20.0%; Pred. No. 2.2e-11;
Matches 167; Conservative 86; Mismatches 264; Indels 319; Gaps 37;
QY 65 EKLNGSVLPGSGAPARLLCRLOAFGETLLLELEQDSGVQVEGLTVQVILGAPPELLGAE 124

A:Molecule type: mRNA
A:Residues: 1-461 <MCK>
A:Experimental source: articular chondrocyte
C:Comment: This protein is a membrane bound protein and involved in cell/cell and cell/m
C:Superfamily: mouse meltrin alpha; disintegrin homology
C:Key words: hydrolase; metalloproteinase; zinc
F:420-503/Domain: disintegrin homology <DIS>
F:348,352,358/Binding site: zinc (His) #status predicted
F:349/Active site: Glu #status predicted

```
Query Match      5.9%; Score 268.5; DB 2; Length 814;
Best Local Similarity 24.3%; Pred. No. 2.2e-10;
Matches 187; Conservative 82; Mismatches 259; Indels 243; Gaps 45;

Qy 34 LVMLLLLLLA-SLLPSARLASPLPR-----EEIVFPEKINGSVLPG-----74
Db 5 LLMALGLLGSPSPS-----WPLPNIGTTEEQAESEKAPREPLEPQVLDLPLSLKKV 60
Qy 75 --SGAPARLLCRLOAFGETLLLELQD-----SGVQV--EGLTVQYLQQA 115
Db 61 LQTSLEPLRIKLELDGDHSHLELQRELVPGRPTLVWYQPDGTRVSEGHTELCVQ 120
Qy 116 PELLGAEPTTY-----LTCINGDPESVASLHWGGALIG-VLQVRGAELHLOPLE 166
Db 121 GRVRGYA--GSWSICTSGRLGLVLTTPERSYTLQPGDLOQPPIISRIQDLHLP--- 175
Qy 167 GGTSPNSAGGPGCAHILRRKSPASGGQPMCNVYKAPLGSPPSPRRRAKRFASLSRPFVTLVVA 226
Db 176 -----GHTCALSWEESVHTQTPP-----EHLPGQRHRRRR--DVVTETKTVELVIVA 221
Qy 227 DDKWAFHAGLRYLLTVMAAAKAFKPSIRN-PVSLVV-----TRVLIG--- 273
Db 222 DHSEA-----QKY-----RDFHLLNRTLEVALLLDFFRPLNVRVALGLEAW 265
Qy 274 SGEISGQVPSAAOTILRSFCAWORGLNTPEDSDPDHEDTALFTRODLQGVSTCDTLGMA 333
Db 266 TQRLVETSPNPAVTLNFWRAHLLPLP-----HDSALVTGTSFSG-----PTVGMA 317
Qy 334 DVGTVCDPARSCAIVEDG---LQSAFTAHELGHVFNMLHD---NSKPCISLNGPLSTS 387
Db 318 IONSICSPDFSGGVNMDHSTSLGVASSIAHELGHSLGLDHLDFGNSCPC---PGPAPAK 374
Qy 388 RHVAPVMAHYD--PEEPWSPCSARFTDFLDNGYGHCLLDK-PEAPLHLPV-TFPGKDY 443
Db 375 TCIME---ASTDFLPLNFSNCSRALEKALLDGMGSLFERLSLP---PMAAFQGNMF 428
Qy 444 -DADRQCOLTFGPSRHCQFPPLPPCAALWCASHLNGHAM-----COTKHSPW----- 489
Db 429 VEPGEQCDGFLDD---C--VDPCCDSLTCQLRPGAQACASDGPCCQNCQLRPSGWQCRPT 483
Qy 490 -----ADGTPCGPAQA-CMGGRCL-HMDOLQDFNIPQAGGWG 524
Db 484 RGDCLDPEFCDSQCPDPSVLSDGEGPCAGQAVCMHGRCASTAAQCCSL----- 534
Qy 525 PWGPMGDCSRTCGGGVQFSRDCTRPVPRNGGKYCEGRRTFRSCNTEDCPTGS--ALTF 582
Db 535 -WGP-----GAQPAAPLCQTANTRG-----NAFGSGGRN--PSGSVWSCPT 573
Qy 583 REEQCAAYNHRITDLFKSPFGPM-----DWPVRYTVAPQDCKLTCQA 625
Db 574 RDAICGQLQCOQTGRTOPLIGSIRDLLWETIDVNGTELNCWVHLDLG---SD----- 622
Qy 626 RALGYVYVLEPRV-VDTGTPCSPDSSVQVQGRCIHAGCDRIIGSKKFKDKC 675
Db 623 -----VAQPLTLLPTGTACGP--GLVCLDHRQCRVD---LLGAQECRSKC 661
```

RESULT 15
A55796
ecarin precursor - saw-scaled viper
C:Species: Echis carinatus (saw-scaled viper)
C:Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 09-Jul-2004
C:Accession: A55796

R:Nishida, S.; Fujita, T.; Kohno, N.; Atoda, H.; Morita, T.; Takeya, H.; Kido, I.; Paine,
Biochemistry 34, 1771-1778, 1995
A:Title: cDNA cloning and deduced amino acid sequence of prothrombin activator (ecarin) f
A:Reference number: A55796; MUID:95151760; PMID:7849037
A:Accession: A55796
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-616 <NIS>
A:Cross-references: UNIPROT:Q90495; GB:D32212; NID:g717090; PIDN:BAA06910.1; PID:g717091
C:Superfamily: mouse meltrin alpha; disintegrin homology
F:404-486/Domain: disintegrin homology <DIS>
F:338/Active site: Glu #status predicted

```
Query Match      5.8%; Score 267; DB 2; Length 616;
Best Local Similarity 22.9%; Pred. No. 2e-10;
Matches 161; Conservative 85; Mismatches 279; Indels 178; Gaps 37;

Qy 37 LLLLLLASLP-----SARLASPLPREBEIVPEKINGSVLPGSAPAR-----LLCR 84
Db 5 LVIICLAVFPVQGGSIILGSGNVNDYEVVYQKV--TALP-KGAVQOQPEQKYEDAMOYE 61
Qy 85 LQAFGETLLLEQDSGVQVVEGLT-VQYLQGAPELL--GGAEPGTYLGTINGDPESVAS 141
Db 62 FEVKGEPVYLHLEKNKELFSEYSETHYSSDDREITNPVEDHCYHGRIONDAESTAS 121
Qy 142 LHWDCGALLGLVQVRGAELHLQPLEGGTPNSAGGPGFAHILRRKSPASGGQ---PWCNV-- 196
Db 122 ISACNG-LKGHFUKGETYFIEPLK--IPDSE---AHAVYKYENIENEDEAPKMGCVTQ 174
Qy 197 -----KAPLGSPPSPRRRAKRFASLSRPFVTLVVDKMAAFH---GAGLKRYLLT 244
Db 175 DNWESDEPKIKTGLIVPHER--KFE--KKFIELVVVVVDHSMVTKYNNDSSTAIRTWIYE 230
Qy 245 VMAAAKAFKPSIRNPVSLVTVILVILSGSEGGVQVPSAAQTILRSFCAMORG--LNTPT 302
Db 231 MLNTVNEIYLPNIR--VALVGLFWCNG---DLINVTSTADDTLHSGEWRASLLNR-- 284
Qy 303 ESDSDPDHFDTAILFTRODLQGVSTCDTLGMADVGVTCDPARSCAIVEDG---LOSFTA 359
Db 285 -----KRHDHAQLLNTVTL---DHSTLGITFVYGMCKSDRSVELILDYSNITFNMYII 335
Qy 360 AHELGHVFNMLHD-----NSKPCISLNGPLSTRHVMAPVMAHYDPEEPWSPCSARFT 413
Db 336 AHMGHSLGMLHDTKFTCGAKPCINFG-----KESIPPPKEFSSCSYDQYN 382
Qy 414 DFLDNGYGHCLLDKP-EAPLHLPVTFPGKDYADRCQQLTFGPDHRHCPQLPPPCALWC 472
Db 383 KYLLKYNPKCILLDPLRKDIASPAVCGNEIWEEGECDCGSPADCRN-----PCDDAATC 437
Qy 473 S---GHLNGHAMCQTVCHSPWADGTPCGPAQACMGGRCLHMDOLQDFNIPQAGGWGPGW 529
Db 438 KLPKGAECNGECCDKCKIRKAGTECRPAR-----467
Qy 530 GDC--SRTCGGVQVFSRDCTRPVPRNGGKYCEGRRTFRSCNTEDCPT-----GS 578
Db 468 DDCDVAEHCTG-----QSAECPRNEFORNGQPC---LNNSGYCVNGDCPIMLNQIALFSP 520
Qy 579 ALTFREEQCAAYNHRITDLF-----KSPFGPMDWVRYTVGVAPOD-QC-KLTQCA 625
Db 521 SATVAQDSCFQRLNQSYYGYCTKEIYGYKRPF-----CAPODVKGGRLYCLD 569
Qy 626 RAL-----GYVYVLEPR--VVDGTPCSPDSSVQVQGRCI 658
Db 570 NSPKGNKRNKNDYSYADENKGIVEPGTKC--EDGKVCINRKCVC 610
```

Search completed: April 1, 2005, 12:52:34
Job time : 55 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 12:34:02 ; Search time 186 Seconds
(without alignments)
2304.356 Million cell updates/sec

Title: US-09-634-287E-2

Perfect score: 4570

Sequence: 1 MSQTSGHPGRGLAGRWLWGA.....LHRRQAQILEILRRPWPAGRK 837

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query	Length	DB	ID	Description
1	4570	100.0	837	1	AT54	HUMAN	Q5173 homo sapien
2	4563	99.8	837	2	Q6UWA8		Q6UWA8 homo sapien
3	4538	99.3	837	2	Q6P4Q8		Q6P4Q8 homo sapien
4	4200	91.9	839	2	Q7YS95		Q7YS95 bos taurus
5	4106	89.8	845	2	Q8BNJ2		Q8BNJ2 mus musculus
6	4105	89.8	833	2	Q8K384		Q8K384 mus musculus
7	3894	85.2	893	2	Q6A017		Q6A017 mus musculus
8	3218	70.4	630	1	AT54	RAT	Q9esp7 rattus norv
9	2161.5	47.3	967	1	AT51	RAT	Q9wuq1 rattus norv
10	2160.5	47.3	967	2	Q68EJ2		Q68EJ2 rattus norv
11	2158	47.2	968	1	AT51	MOUSE	Q97857 mus musculus
12	2135	46.7	967	1	AT51	HUMAN	Q9uh18 homo sapien
13	2127	46.5	967	2	Q8NE26		Q8NE26 homo sapien
14	1998.5	43.7	759	2	Q8HZM8		Q8HZM8 equus cabal
15	1915	41.9	950	1	AT15	HUMAN	Q8te58 homo sapien
16	1842.5	40.3	900	1	AT58	HUMAN	Q9up79 homo sapien
17	1824	39.9	905	1	AT58	MOUSE	P59110 mus musculus
18	1659	36.3	339	2	Q8NEK2		Q8NEK2 homo sapien
19	1576	34.5	930	1	AT55	MOUSE	Q9r001 mus musculus
20	1567.5	34.3	928	2	Q6TV19		Q6TV19 rattus norv
21	1558	34.1	930	1	AT55	HUMAN	Q9una0 homo sapien
22	1547	33.9	1306	1	AT20	MOUSE	P59511 mus musculus
23	1518.5	33.2	867	2	Q66KM3		Q66KM3 xenopus tro
24	1494.5	32.7	1935	1	AT59	HUMAN	Q9p2n4 homo sapien
25	1482	32.4	1911	1	AT20	HUMAN	P59510 homo sapien
26	1386.5	30.3	623	2	Q8BGP4		Q8BGP4 m mus muscu
27	1317	28.8	2165	2	Q19791		Q19791 caenorhabdi
28	1217	26.6	245	1	AT54	BOVIN	Q9tce93 bos taurus
29	1150	25.2	562	1	AT15	MOUSE	P59384 mus musculus
30	1091.5	23.9	1077	1	AT10	HUMAN	Q9h324 homo sapien
31	1087	23.8	192	2	Q95N24		Q95N24 equus cabal

RESULT 1

ID AT54 HUMAN STANDARD; PRT; 837 AA.
AC Q75173; Q9UN83;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE ADAMTS-4 precursor (EC 3.4.24.82) (A disintegrin and metalloproteinase with thrombospondin motifs 4) (ADAM-TS 4) (ADAM-TS4) (Aggrecanase 1) (ADMP-1).
DE Name=ADAMTS4; Synonyms=KIAA0688;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98403880; PubMed=9734811;
RA Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
RA "Prediction of the coding sequences of unidentified human genes. X. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.";
RL DNA Res. 5:169-176(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99286303; PubMed=10356395; DOI=10.1126/science.284.5420.1664;
RA Tortorella M.D., Burn T.C., Pratta M.A., Abbaszade I., Hollis J.M., Liu R.-Q., Rosenfeld S.A., Copeland R.A., Decicco C.P., Wynn R., Rockwell A., Yang F., Duke J.L., Solomon K., George H., Bruckner R., Nagase H., Itoh Y., Ellis D.M., Ross H., Wiswall B.H., Murphy K., Hillman M.C. Jr., Hollis G.P., Newton R.C., Magolda R.L., Trzaskos J.M., Arner E.C.;
RA "Purification and cloning of aggrecanase-1: a member of the ADAMTS family of proteins.";
RL Science 284:1664-1666(1999).
RN [3]
RP SEQUENCE FROM N.A.
RA Sawaji Y., Nagase H., Saklatvala J., Clark A.R.;
RL "ADAMTS-4 genomic locus.";
RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP PARTIAL SEQUENCE, AND CHARACTERIZATION.
RX MEDLINE=20400518; PubMed=10827174; DOI=10.1074/jbc.M001065200;
RA Tortorella M.D., Pratta M.A., Liu R.-Q., Abbaszade I., Ross H., Burn T.C., Arner E.C.;
RT "The thrombospondin motif of aggrecanase-1 (ADAMTS-4) is critical for aggrecan substrate recognition and cleavage.";
RL J. Biol. Chem. 275:25791-25797(2000).
CC -!- FUNCTION: Cleaves aggrecan, a cartilage proteoglycan, and may be involved in its turnover. May play an important role in the destruction of aggrecan in arthritic diseases. Could also be a critical factor in the exacerbation of neurodegeneration in

ALIGNMENTS

CC Alzheimer's disease. Cleaves aggrecan at the 392-Glu-|-Ala-393 site.

CC -1- CATALYTIC ACTIVITY: Glutamyl endopeptidase; bonds cleaved include 370-Thr-Glu-Gly-Glu-|-Ala-Arg-Gly-Ser-377 in the interglobular domain of mammalian aggrecan.

CC -1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).

CC -1- SUBCELLULAR LOCATION: Secreted. Associated with the extracellular matrix (By similarity).

CC -1- TISSUE SPECIFICITY: Expressed in brain, lung and heart. Expressed at very low level in placenta and skeletal muscles.

CC -1- INDUCTION: By interleukin-1.

CC -1- DOMAIN: The spacer domain and the TSP type-1 domains are important for a tight interaction with the extracellular matrix.

CC -1- PTM: The precursor is cleaved by a furin endopeptidase.

CC -1- SIMILARITY: Belongs to the peptidase M12B family.

CC -1- SIMILARITY: Contains 1 disintegrin-like domain.

CC -1- SIMILARITY: Contains 1 TSP type-1 domain.

CC -1- CAUTION: Has sometimes been referred to as ADAMTS2.

CC -----

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CC -----

DR EMBL; AB014588; BAA31663.2; ALT_INIT.

DR EMBL; AF148213; AAD41494.1; -.

DR EMBL; AY044847; AAL02262.1; -.

DR PIR; T00355; T00355.

DR HSSP; P07996; 1LSL.

DR MEROPS; M12.221; -.

DR Genew; HGNC:220; ADAMTS4.

DR MIM; 603876; -.

DR GO; GO:0008237; P:metallopeptidase activity; TAS.

DR GO; GO:0006508; P:proteolysis and peptidolysis; TAS.

DR GO; GO:0001501; P:skeletal development; TAS.

DR InterPro; IPR010294; ADAM_spacer1.

DR InterPro; IPR001762; Disintegrin.

DR InterPro; IPR006025; Pept_M_Zn_BS.

DR InterPro; IPR001590; Peptidase_M12B.

DR InterPro; IPR000884; TSP1.

DR InterPro; IPR008085; TSP1.

DR Pfam; PF05986; ADAM_spacer1; 1.

DR Pfam; PF01421; ReprGlysin; 1.

DR Pfam; PF00090; TSP_1; 1.

DR PRINTS; PR01705; TSP1REPEAT.

DR SMART; SM00209; TSP1; 1.

DR PROSITE; PS50215; ADAM_MEPRO; 1. FALSE_NEG.

DR PROSITE; PS00427; DISINTEGRIN_1; FALSE_NEG.

DR PROSITE; PS0214; DISINTEGRIN_2; FALSE_NEG.

DR PROSITE; PS50092; TSP1; 1.

DR PROSITE; PS00142; ZINC_PROTEASE; 1.

KW Direct protein sequencing; Extracellular matrix; Glycoprotein;

KW Hydroxylase; Metalloproteinase; Signal; Zinc; Zymogen.

FT SIGNAL 1 51 Potential.

FT PROPEP 52 212

FT CHAIN 213 837

FT DOMAIN 213 436 Metalloprotease.

FT DOMAIN 437 519 Disintegrin-like.

FT DOMAIN 520 575 TSP type-1.

FT DOMAIN 577 685 Cys-rich.

FT DOMAIN 686 837 Spacer.

FT DOMAIN 247 252 Poly-Ala.

FT SITE 194 194 Cysteine switch (Potential).

FT METAL 361 361 Zinc (catalytic) (By similarity).

FT ACT_SITE 362 362 By similarity.

FT METAL 365 365 Zinc (catalytic) (By similarity).

FT METAL 371 371 Zinc (catalytic) (By similarity).

FT CARBOHYD 68 68 N-linked (GlcNAc...) (Potential).

FT CONFLICT 77 77 A -> T (in Ref. 1).

FT CONFLICT 626 626 R -> Q (in Ref. 3).

FT	CONFLICT	682		G -> R (in Ref. 3).	
SQ	SEQUENCE	837	AA; 90224	MM; 5DF9C9AC137DF41F	CRC64;
	Query Match		100.0%;	Score 4570;	DB 1; Length 837;
	Best Local Similarity		100.0%;	Pred. No. 4.7e-286;	
	Matches	837;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
QY	1	MSQTGSHPGGLAGRWLWGAQPCLLLPVPLSWLWLLLLASLPASRLAPLPREEE	60		
DB	1	MSQTGSHPGGLAGRWLWGAQPCLLLPVPLSWLWLLLLASLPASRLAPLPREEE	60		
QY	61	IVFPEKLINGSVPGSGAPARLLCQLQAFGETLLLELEQDSGVQVEGLTVQYLQAPLLG	120		
DB	61	IVFPEKLINGSVPGSGAPARLLCQLQAFGETLLLELEQDSGVQVEGLTVQYLQAPLLG	120		
QY	121	GAEFGTYLTGTINGDPESVASLHWGCGALLGVLYQGAELHQLQPLEGCTPNSAGGPGAH	180		
DB	121	GAEFGTYLTGTINGDPESVASLHWGCGALLGVLYQGAELHQLQPLEGCTPNSAGGPGAH	180		
QY	181	LRRKSPASGQCPMNCVAPLGSPPRRRAKRFASLSRFVETLVVADDKMAAFHAGLKR	240		
DB	181	LRRKSPASGQCPMNCVAPLGSPPRRRAKRFASLSRFVETLVVADDKMAAFHAGLKR	240		
QY	241	YLLTMAAAAKAFKHPISIRNPVSLVTRLVILSGERGPGVPSAAOTLRSFCAWQRLN	300		
DB	241	YLLTMAAAAKAFKHPISIRNPVSLVTRLVILSGERGPGVPSAAOTLRSFCAWQRLN	300		
QY	301	TPEDSDPDHFDTAILFTQDLICGVSTCTDLGADVTVCDPAPSCAIVEDDGLQSAFTAA	360		
DB	301	TPEDSDPDHFDTAILFTQDLICGVSTCTDLGADVTVCDPAPSCAIVEDDGLQSAFTAA	360		
QY	361	HELGHVFNMLHDNSKPCISLNGPLSTSRHVMAVMAHVDPEEPWSPCSARITFDLDNGY	420		
DB	361	HELGHVFNMLHDNSKPCISLNGPLSTSRHVMAVMAHVDPEEPWSPCSARITFDLDNGY	420		
QY	421	GHCLLDKPEAPLHLVTPFGKDYDADROCOLTEGDSRHCPLPPPCAAALWCSGHLNGHA	480		
DB	421	GHCLLDKPEAPLHLVTPFGKDYDADROCOLTEGDSRHCPLPPPCAAALWCSGHLNGHA	480		
QY	481	MCQTKHSPWADGTPCGPAQACMGGRCLHMDQLQDNIFPAQGWGPMWGDGCSRTCGGV	540		
DB	481	MCQTKHSPWADGTPCGPAQACMGGRCLHMDQLQDNIFPAQGWGPMWGDGCSRTCGGV	540		
QY	541	QFSRDCTRPVPRNGKCYCEGRTFRSCNTEDECTGSAITFREECQCAYNHRTDLKSF	600		
DB	541	QFSRDCTRPVPRNGKCYCEGRTFRSCNTEDECTGSAITFREECQCAYNHRTDLKSF	600		
QY	601	PGMDWVPRTYTGAPODQCKLTQARALGYVYVLEPRVVDGTPCSPDSSSVCQGRCIHA	660		
DB	601	PGMDWVPRTYTGAPODQCKLTQARALGYVYVLEPRVVDGTPCSPDSSSVCQGRCIHA	660		
QY	661	GCDRIIGSKKFKDKMVCQDGGSGCSKQSGSFRKFRYGVNNVVTIPAGATHILVROQGNP	720		
DB	661	GCDRIIGSKKFKDKMVCQDGGSGCSKQSGSFRKFRYGVNNVVTIPAGATHILVROQGNP	720		
QY	721	GHRISYIALKLDPGSAVALNGEYTLMPSTDDVLPAGAVSLRYSGATAASTLSHGGLAQP	780		
DB	721	GHRISYIALKLDPGSAVALNGEYTLMPSTDDVLPAGAVSLRYSGATAASTLSHGGLAQP	780		
QY	781	LTQLQVLVAGNPQDTRLRYSPFFVPRPTFPPTQDMLHRRRAQILFILLRRRPMWGRK	837		
DB	781	LTQLQVLVAGNPQDTRLRYSPFFVPRPTFPPTQDMLHRRRAQILFILLRRRPMWGRK	837		
RESULT 2					
Q6UWAS PRELIMINARY; PRT; 837 AA.					
ID	Q6UWAS				
AC	Q6UWAS				
DT	05-JUL-2004	(TrEMBLrel. 27, Created)			
DT	05-JUL-2004	(TrEMBLrel. 27, Last sequence update)			
DT	05-JUL-2004	(TrEMBLrel. 27, Last annotation update)			
DE	ADAMTS4				
GN	ORFNames=UNQ769;				

DR GO: 0007229; P.integrin-mediated signaling pathway; IEA.
 DR GO: 0006508; P.proteolysis and peptidolysis; IEA.
 DR InterPro: IPR006586; ADAM cysteine.
 DR InterPro: IPR010294; ADAM spacer1.
 DR InterPro: IPR001590; Peptidase M12B.
 DR InterPro: IPR006025; Pept_M_Zn_BS.
 DR InterPro: IPR000884; TSP1.
 DR InterPro: IPR008085; TSP1.
 DR Pfam: PF05986; ADAM_spacer1; 1.
 DR Pfam: PF01421; Reprolysin; 1.
 DR Pfam: PF00090; TSP1; 1.
 DR PRINTS: PR01705; TSP1REPEAT.
 DR SMART: SM00209; TSP1; 1.
 DR SMART: PS00215; ADAM_MEPRO; 1.
 DR PROSITE: PS00092; TSP1; 1.
 DR PROSITE: PS00142; ZINC_PROTEASE; UNKNOWN_1.
 KW Integrin.
 SQ SEQUENCE 837 AA; 90149 MW; 3B91C651E54EFC5F CRC64;
 Query Match 99.3%; Score 4538; DB 2; Length 837;
 Best Local Similarity 99.3%; Pred. No. 5.4e-284;
 Matches 831; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 MSQTGSHPGRLAGRWLWGAQPCLLIPVPLSWMLLLLLASLLPSARLASPLPRE 60
 Db 1 MSQIGSHPGRLAGRWLWGAQPCLLIPVPLSWMLLLLLASLLPSARLASPLPRE 60
 Qy 61 IVFPEKLSVLPQSGAPARLLCLOAFGETLLLELQDSGVQVEGLTVQYLQAPPELLG 120
 Db 61 IVFPEKLSVLPQSGAPARLLCLOAFGETLLLELQDSGVQVEGLTVQYLQAPPELLG 120
 Qy 121 GAEPGTLYLTGTINDGPESVSLHWDGGLLGVLYRGAELHLOPLEGTPNSAGGCAHI 180
 Db 121 GAEPGTLYLTGTINDGPESVSLHWDGGLLGVLYRGAELHLOPLEGTPNSAGGCAHI 180
 Qy 181 LRRKSPASGQPMCNVAPLIGSPSPRRRAKRFASLRFVETLVVADKMAAFHAGLKR 240
 Db 181 LRRKSPASGQPMCNVAPLIGSPSPRRRAKRFASLRFVETLVVADKMAAFHAGLKR 240
 Qy 241 YLLTWMAAAKAFKHPSTIRNPVSLVWTRVLTLGSGEGPQVGPAAQTLRSFCAWQGLN 300
 Db 241 YLLTWMAAAKAFKHPSTIRNPVSLVWTRVLTLGSGEGPQVGPAAQTLRSFCAWQGLN 300
 Qy 301 TPESDDPHFDFTAILFTQDLGCVSTCDTLGMADVGTCDPARCAIVEDDGLQSAFTA 360
 Db 301 TPESDDPHFDFTAILFTQDLGCVSTCDTLGMADVGTCDPARCAIVEDDGLQSAFTA 360
 Qy 361 HELGHVFNVLHNDNSKPCI SLNGPLSTSRHVMAPVMAHVDPEEPWSPCSARFITDPLNGY 420
 Db 361 HELGHVFNVLHNDNSKPCI SLNGPLSTSRHVMAPVMAHVDPEEPWSPCSARFITDPLNGY 420
 Qy 421 GHCLDKPEAPLHLVPTFGKYDADRCQLTFFGDSRHCPQLPPPCAALWCSGHLNGHA 480
 Db 421 GHCLDKPEAPLHLVPTFGKYDADRCQLTFFGDSRHCPQLPPPCAALWCSGHLNGHA 480
 Qy 481 MCQTKHSPWADTGPCGPAQA CMGRCCLHMDQLQDNIPQAGGPGWPGWDCSRTCCGGV 540
 Db 481 MCQTKHSPWADTGPCGPAQA CMGRCCLHMDQLQDNIPQAGGPGWPGWDCSRTCCGGV 540
 Qy 541 QFSRRDCTRPVPRNGKCYCEGRRTFRSCNTDCTGSAITFREQCAYNHRITDLFKSF 600
 Db 541 QFSRRDCTRPVPRNGKCYCEGRRTFRSCNTDCTGSAITFREQCAYNHRITDLFKSF 600
 Qy 601 PGFMWVPRYTVGAPQDQKLCQARALGYVYVLEPRVVDGTPCSPDSSSVQVGRCLHA 660
 Db 601 PGFMWVPRYTVGAPQDQKLCQARALGYVYVLEPRVVDGTPCSPDSSSVQVGRCLHA 660
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Db 721 GHRSIYLALKLPGSYALNGEYTLMPSPDVTVDVLPAGVSLRYSGATAASETLSHGGLAQP 780
 Qy 781 LTLQVLVAGNPQDTRLFYSFFVPRPTSTPRTPQDWLHRRRAQLLEILRRRPWAGRK 837
 Db 781 LTLQVLVAGNPQDTRLFYSFFVPRPTSTPRTPQDWLHRRRAQLLEILRRRPWAGRK 837
 RESULT 4
 QYYS95 PRELIMINARY; PRT; 839 AA.
 ID QYYS95
 AC QYYS95; TREMBLrel. 25, Created)
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
 DE 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE AggreCanase-1.
 GN Name=ADAMTS-4;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Arai M., Anderson D., Annis B., Collins-Racie L., Corcoran C.,
 RA DiBlasio-Smith E., Morris E., Dornier A., LaVallie E.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF516915; AAP47196.1; -.
 DR HSSP; P83512; INDI.
 DR GO: 0004222; F:metalloendopeptidase activity; IEA.
 DR GO: 0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro: IPR010294; ADAM spacer1.
 DR InterPro: IPR001590; Peptidase M12B.
 DR InterPro: IPR006025; Pept_M_Zn_BS.
 DR InterPro: IPR000884; TSP1.
 DR Pfam: PF05986; ADAM_spacer1; 1.
 DR Pfam: PF01421; Reprolysin; 1.
 DR SMART: SM00209; TSP1; 1.
 DR PROSITE: PS00215; ADAM_MEPRO; 1.
 DR PROSITE: PS00092; TSP1; 1.
 DR PROSITE: PS00142; ZINC_PROTEASE; UNKNOWN_1.
 SQ SEQUENCE 839 AA; 90279 MW; 1B488A27DF5B96B1 CRC64;
 Query Match 91.9%; Score 4200; DB 2; Length 839;
 Best Local Similarity 91.8%; Pred. No. 3.3e-262;
 Matches 772; Conservative 25; Mismatches 38; Indels 6; Gaps 3;
 Qy 1 MSQTGSHPGRLAGRWLWGAQPCLLIPVPLSW--LWMLLLLLASLLPSARLASPLPRE 58
 Db 1 MSHMDSHPGRLAGRWLWGIQPRLLPTVPVSGSLVW--LWMLLLPSANPASPDLPRE 58
 Qy 59 EEIVFPEKLSVLPQSGAPARLLCLOAFGETLLLELQDSGVQVEGLTVQYLQAPEL 118
 Db 59 EEIVFPEKLSVLPQSGAPARLLYELPAFGETLLLELQDSGVQVEGLTVQYLQAPEL 118
 Qy 119 LGGAEPGTLYLTGTINDGPESVSLHWDGGLLGVLYRGAELHLOPLEGTPNSAGGCA 178
 Db 119 LGGAEPGTLYLTGTINDGPESVSLHWDGGLLGVLYRGAELHLOPLEGTPNSAGGCA 178
 Qy 179 HILRRKSPASGQPMCNVAPLIGSPSPRRRAKRFASLRFVETLVVADKMAAFHAGL 238
 Db 179 HILRRKSPVSGQPMCNVAPLIGSPSPRRRAKRFASLRFVETLVVADKMAAFHAGL 238
 Qy 239 KRYLLTWMAAAKAFKHPSTIRNPVSLVWTRVLTLGSGEGPQVGPAAQTLRSFCAWQ 298
 Db 239 KRYLLTWMAAAKAFKHPSTIRNPVSLVWTRVLTLGSGEGPQVGPAAQTLRSFCAWQ 298
 Qy 299 LNTPEDSDPHFDFTAILFTQDLGCVSTCDTLGMADVGTCDPARCAIVEDDGLQSAFT 358
 Db 299 LNTPDADPHFDFTAILFTQDLGCVSTCDTLGMADVGTCDPARCAIVEDDGLQSAFT 358
 Qy 359 AAHELGHVFNVLHNDNSKPCI SLNGPLSTSRHVMAPVMAHVDPEEPWSPCSARFITDPLDN 418

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Db 359 ANHELGHVFMHNDNSKQCTGLNGPESTSRVNAFVMAHVDPEEPWSPCSARFTITDFLDN 418
QY 419 GYGHCLLDKPEALPHLPVTFPGKDYADROCOQTFFGDSRHCQLPPLPPCAALWCSGHLNG 478
Db 419 GFHCLLDKPEALPHLPVTFPGKDYADROCOQTFFGDSRHCQLPPLPPCAALWCSGHLNG 478
QY 479 HAMCQTKHSPWADGTPCGPAQACMGGRCLHMDQLQDFNIPQAGGWPWGDCSRCTCGG 538
Db 479 HAMCQTKHSPWADGTPCGPAQACMGGRCLHMDQLQDFNIPQAGGWPWGDCSRCTCGG 538
QY 539 GVQFSSRDCTRPVPRNGKCYCEGRTRFRSCNTDCTGTSALTRFREOCAYNHRDLPFK 598
Db 539 GVQFSSRDCTRPVPRNGKCYCEGRTRFRSCNTDCTGTSALTRFREOCAYNHRDLPFK 598
QY 599 SPFGPMWVPRYTGVAPODOCKLTQCARALGYTVVLEPRVVDGTPCSPDSSSVCVQGRCI 658
Db 599 NFGPMWVPRYTGVAPODOCKLTQCARALGYTVVLEPRVVDGTPCSPDSSSVCVQGRCI 658
QY 659 HAGCDRIIGSKKKFKDKCMWCGDGGSCGSKGSGFRFRYGYNNVVTPAGATHILVRQOG 718
Db 659 HAGCDRIIGSKKKFKDKCMWCGDGGSCGSKGSGFRFRYGYNNVVTPAGATHILVRQOG 718
QY 719 NPGHRIYLLKLPDGSYALNGEYTLMPSTDVLPQAVSLRYSYGATAASETLSGHGPLA 778
Db 719 SPSVRSLLYLLKLPDGSYALNGEYTLMPSTDVLPQAVSLRYSYGATAASETLSGHGPLA 778
QY 779 QPILTQVLVAGNPQDRLRYSFFV--PRPTSTPRTPQDMLHRRRAQILEILRRRWPAGR 836
Db 779 EPTLTQVLVAGNPQDRLRYSFFV--PRPTSTPRTPQDMLHRRRAQILEILRRRWPAGR 838
QY 837 K 837
Db 839 K 839

RESULT 5
Q8BNJ2 PRELIMINARY; PRT; 845 AA.
AC Q8BNJ2;
DT Q1-MAR-2003 (T-EMBLrel. 23, Created)
DT Q1-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT Q1-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Mus musculus 9 days embryo whole body cDNA, RIKEN full-length enriched
DE library, clone:D030041M02 product:a disintegrin-like and
DE metalloprotease (repolysin type) with thrombospondin type 1 motif, 4,
DE full insert sequence.
GN Name=Adams4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=9927253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
[2]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[3]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RA The FANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
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RL Nature 420:563-573(2002).
[4]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
[5]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[6]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX STRAIN=C57BL/6J; Adants4.
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kouda M., Koya S.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Kura M.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akaiura S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK083534; BAC38944.1; -.
DR HSSP; P07996; ILSL.
DR MEROPS; M12.221; -.
DR MGD; MGI:1339949; Adants4.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0007229; P:integrin-mediated signaling pathway; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR010294; ADAM_spacer1.
DR InterPro; IPR001590; Peptidase_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008085; TSP_1.
DR Pfam; PF05986; ADAM_spacer1; 1.
DR Pfam; PF01421; Repolysin; 1.
DR Pfam; PF00090; TSP_1; 1.
DR PRINTS; PR01705; TSP1REPEAT.
DR SMART; SM00209; TSP1; 1.
DR PROSITE; PS00215; ADAM_MEPRO; 1.
DR PROSITE; PS00092; TSP1; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
DR Integrin; Metalloprotease; Protease.
SQ SEQUENCE 845 AA; 91238 MW; B496C3190D1A9225 CRC64;
Query Match 89.8%; Score 4106; DB 2; Length 845;
Best Local Similarity 90.5%; Pred. No. 3.8e-256;
Matches 758; Conservative 22; Mismatches 52; Indels 6; Gaps 2;
QY 1 MSQTGSHPGRGLAGRWLWGAQPCLLPIVPLSVLWMLLLLLASLPASLPAPREE 60
Db 13 MSQMGHPRRLTGHWRQPCPL-----PLHTVQWRRLLLAFLLSLAWPASPREE 67
QY 61 IVPPEKING-SVLPQSGAPARLLCRQAGETLLLEQDSGVQVVEGLTVQYLGQAPELL 119
Db 68 IVPPEKINGSSILPGSGVPARLLYRLPAFGEMLLLEQDPGVQVEGLTVQYLGQAPML 127
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QY	120	GGAEPTGTYLTGTINGDPESVASLHWDGALLGVLYRGAEHLQPLEGGTPNSAGGPGAH	179
DB	128	GGAEPTGTYLTGTINGDPESVASLHWDGALLGVLYRGAEHLQPLEGGTPNSAGGPGAH	187
QY	180	ILRRKSPASQGGPNCVAPLSPSPRRPRRAKRFASLSRFVETLVVADDKMAAFHGAGLK	239
DB	188	ILRRKSPASQGGPNCVAPLSPSPRRPRRAKRFASLSRFVETLVVADDKMAAFHGAGLK	247
QY	240	RYLLTVMAAAAKAFKPSIRNPVSLVTRVLVILSGEGEPQVGPSSAAQTLSFCFAWQGL	299
DB	248	RYLLTVMAAAAKAFKPSIRNPVSLVTRVLVILSGEGEPQVGPSSAAQTLSFCFAWQGL	307
QY	300	NTPEDSDPHFDFTAILFTRODLGCVSTCDTLGMADVGTVCDPARSCAIVEDDGLQSAFTA	359
DB	308	NTPEDSDPHFDFTAILFTRODLGCVSTCDTLGMADVGTVCDPARSCAIVEDDGLQSAFTA	367
QY	360	AHELGHVFNMLHDSKPCISLNGPLSTSRHVMAFVMAHVDPPEPWPSCSARFITDFLDNG	419
DB	368	AHELGHVFNMLHDSKPCISLNGPLSTSRHVMAFVMAHVDPPEPWPSCSARFITDFLDNG	427
QY	420	YGHCLLDKPEAPLHLPVTTPGKYDADROCOLTFGPDSDRHCPOLPFPCAALWCSGHLNGH	479
DB	428	YGHCLLDKPEAPLHLPVTTPGKYDADROCOLTFGPDSDRHCPOLPFPCAALWCSGHLNGH	487
QY	480	AMCQTKHSPWADGTPFCGPAQACMGRCCLHMDQLODFNIPOAGGWPWGPWGDSCSRTCGGG	539
DB	488	AMCQTKHSPWADGTPFCGPAQACMGRCCLHMDQLODFNIPOAGGWPWGPWGDSCSRTCGGG	547
QY	540	VQFSRDCTRPVPRNGKCYCEGRTRFRSNTEDCPTGSAITPREEOCAAYNHTDLFKS	599
DB	548	VQFSRDCTRPVPRNGKCYCEGRTRFRSNTEDCPTGSAITPREEOCAAYNHTDLFKS	607
QY	600	PPGMDWVPRVTGVAPODOCKLTQARALGYVYVLEPRVVDGTPCSDPSVSVQGRCIH	659
DB	608	PPGMDWVPRVTGVAPODOCKLTQARALGYVYVLEPRVVDGTPCSDPSVSVQGRCIH	667
QY	660	AGCDRIIGSKKKFKCMVCGGSGCSKQSGFRKFRYGNVVTIIPAGATHILVROQGN	719
DB	668	AGCDRIIGSKKKFKCMVCGGSGCSKQSGFRKFRYGNVVTIIPAGATHILVROQGN	727
QY	720	PHRSIYIALKLPGSGYALNGEYTLMPSPDTDWLPVGLVSLYSGATASETLSHGFLAQ	779
DB	728	SGLSKIYIALKLPGSGYALNGEYTLMPSPDTDWLPVGLVSLYSGATASETLSHGFLAQ	787
QY	780	PLTLQVLVAGNPQDTRLSYFVPRPTSTPRPTQDWLHRAQILEILRRPWPAGRK	837
DB	788	PLTLQVLVAGNPQDTRLSYFVPRPTSTPRPTQDWLHRAQILEILRRPWPAGRK	845
RESULT 6			
Q8K384			
ID	Q8K384	PRELIMINARY; PRT; 833 AA.	
AC	Q8K384;		
DT	01-OCT-2002 (TrEMBLrel. 22, Created)		
DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)		
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)		
DE	Adams4 protein.		
GN	Name=Adams4;		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RC	SEQUENCE FROM N.A.		
RC	STRAIN=FVB/N; TISSUE=Mammary tumor. C3;		
RX	MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;		
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,		
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,		
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,		
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,		
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,		
RA	Rana S.S., Ioquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,		
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,		
RA	Villalón D.K., Muzny E., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,		
RA	Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,		
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		
RA	Blakesley R.M., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,		
RA	Krzywinski M.I., Skalska U., Smailus D.B., Schnerch A., Schein J.E.,		
RA	Jones S.J., Marra M.A.;		
RT	"Generation and initial analysis of more than 15,000 full-length human		
RT	and mouse cDNA sequences.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=FVB/N; TISSUE=Mammary tumor. C3;		
RA	Strausberg R.;		
RL	Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; BC027773; AAH27773.1; -.		
DR	HSSP; P07996; 1LSL.		
DR	MEROFS; M12.221; -.		
DR	MGI; M1339949; Adams4.		
DR	GO; GO:0004222; F:metalloendopeptidase activity; IEA.		
DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.		
DR	InterPro; IPR010294; ADAM spacer1.		
DR	InterPro; IPR001590; Peptidase M12B.		
DR	InterPro; IPR006025; Pept. M_Zn_BS.		
DR	InterPro; IPR000884; TSP1_		
DR	InterPro; IPR008085; TSP.1.		
DR	Pfam; PF05986; ADAM_spacer1; 1.		
DR	Pfam; PF01421; Reprolysin; 1.		
DR	Pfam; PF00090; TSP.1; 1.		
DR	PRINTS; PR01705; TSP1REPEAT.		
DR	SMART; SM00209; TSP1.1.		
DR	PROSITE; PS00215; ADAM_MPRO; 1.		
DR	PROSITE; PS00992; TSP1; 1.		
DR	PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN 1.		
SQ	SEQUENCE 833 AA; 90097 MW; 4CEC83DFBC3AA619 CRC64;		
Query Match 89.8%; Score 4105; DB 2; Length 833;			
Best Local Similarity 90.5%; Pred. No. 4.4e-256;			
Matches 758; Conservative 22; Mismatches 52; Indels 6; Gaps 2;			
QY	1	MSQSGHPGRGLAGRWLGAQPCILLPIVPLSWLWLLILLASLPSARLASPLREE	60
DB	1	MSQGLHPRGLTGHWRFPCL-----PLHTVQWRLLLLAFLLSLWAPSLREE	55
QY	61	IVFPEKING-SVLPGSGAPARLLCRLOAFGETLLLEQDSGVQVVEGLTVQYLGAPELL	119
DB	56	IVFPEKINGSSILPGSGVPARLLYRLPAFGEMLLLEQDPGVQVVEGLTVQYLGAPEML	115
QY	120	GGABPGTYLTGTINGDPESVASLHWDGALLGVLYRGAEHLQPLEGGTPNSAGGPGAH	179
DB	116	GGABPGTYLTGTINGDPESVASLHWDGALLGVLYRGAEHLQPLEGGTPNSAGGPGAH	175
QY	180	ILRRKSPASQGGPNCVAPLSPSPRRPRRAKRFASLSRFVETLVVADDKMAAFHGAGLK	239
DB	176	ILRRKSPASQGGPNCVAPLSPSPRRPRRAKRFASLSRFVETLVVADDKMAAFHGAGLK	235
QY	240	RYLLTVMAAAAKAFKPSIRNPVSLVTRVLVILSGEGEPQVGPSSAAQTLSFCFAWQGL	299
DB	236	RYLLTVMAAAAKAFKPSIRNPVSLVTRVLVILSGEGEPQVGPSSAAQTLSFCFAWQGL	295
QY	300	NTPEDSDPHFDFTAILFTRODLGCVSTCDTLGMADVGTVCDPARSCAIVEDDGLQSAFTA	359
DB	296	NTPEDSDPHFDFTAILFTRODLGCVSTCDTLGMADVGTVCDPARSCAIVEDDGLQSAFTA	355
QY	360	AHELGHVFNMLHDSKPCISLNGPLSTSRHVMAFVMAHVDPPEPWPSCSARFITDFLDNG	419
DB	356	AHELGHVFNMLHDSKPCISLNGPLSTSRHVMAFVMAHVDPPEPWPSCSARFITDFLDNG	415
QY	420	YGHCLLDKPEAPLHLPVTTPGKYDADROCOLTFGPDSDRHCPOLPFPCAALWCSGHLNGH	479


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Db 416 YGCHLLDKPEAPLHLPATPGKDYADROQCLTFGPDSSHCPQLPPPCAAALMCSGHLNGH 475
QY 480 AMQCTKHSFWADGTPCGPAQACMGGRCLHMDQLQDENIPQAGGWPWGWDGDCSRCTCGGG 539
Db 476 AMQCTKHSFWADGTPCGSQAQCMGGRCLHVDQLQDFNVPQAGGWPWGWDGDCSRCTCGGG 535
QY 540 VPFSSRDCTRPVPRNGGKYCEGRTFRSCNTDCTGTSALTFRBQCAAYNHRDTLFXS 599
Db 536 VPFSSRDCTRPVPRNGGKYCEGRTFRSCNTDCTGTSALTFRBQCAAYNHRDTLFXS 595
QY 600 FPGPMDWPRYTGVAPODCKLTCQARALGYVYVLEPRVVDGTPCSPDSSVVCQGRCH 659
Db 596 FPGPMDWPRYTGVAPODCKLTCQARALGYVYVLEPRVVDGTPCSPDSSVVCQGRCH 655
QY 660 AGCDRIIGSKKPKDKMVCGGDGGSGSKSGSPKRYGYNVVTIPAGATHILVQOQN 719
Db 656 AGCDRIIGSKKPKDKMVCGGDGGSGSKSGSPKRYGYSVDVVTIPAGATHILVQOQN 715
QY 720 PGHRSYIALKLPDGSYALNGEYTLMPSPDVLPGAVSLRYSGATAASETLSGHGFLAQ 779
Db 716 SGLKSYIALKLPDGSYALNGEYTLMPSPDVLPGAVSLRYSGATAASETLSGHGFLAQ 775
QY 780 PLTLQVLVAGNPQDTRLRYSFFVPRTPSTPRTPQDWLHRAQIILEILRRPWAQRK 837
Db 776 PLTLQVLVAGNPQARLRYSFFVPRVPTPRPPQDWLQRRABEILKLRKPWAQRK 833

RESULT 7
Q6A017 PRELIMINARY; PRT; 893 AA.
ID AC Q6A017;
DC 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE MKIA0688 protein (Fragment).
GN Name=MKIA0688;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_205-218(2004).
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Okazaki N., Kikuno R.F., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
RA Saga Y., Seino S., Nishimura M., Kaisho T., Hoshino K., Kitamura H.,
RA Nagase T., Ohara O., Koga H.;
RT "Prediction of the Coding Sequences of Mouse Homologues of KIAA Gene:
RT IV. The Complete Nucleotide Sequences of 500 Mouse KIAA-Homologous
RT cDNAs Identified by Screening of Terminal Sequences of cDNA Clones
RT Randomly Sampled from Size-Fractionated Libraries.";
RL DNA Res. 11:205-218(2004).
DR EMBL; AK173001; BAD32279.1; -.
DR GO; GO:004222; F:metallopeptidase activity; IEA.
DR GO; GO:006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR006586; ADAM cysteine.
DR InterPro; IPR010294; ADAM spacer1.
DR InterPro; IPR001590; Peptidase M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR000885; TSP1.
DR Pfam; PF05986; ADAM spacer1; 1.
DR Pfam; PF01421; Reprolysin; 1.
DR Pfam; PF00090; TSP1; 1.
DR PRINTS; PR01705; TSP1REPEAT.
DR SMART; SM00608; ACR; 1.
DR SMART; SM00209; TSP1; 1.
DR PROSITE; PS0215; ADAM MEPRO; 1.
DR PROSITE; PS0092; TSP1; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 893 AA; 96389 MW; F4F12254E2CCFA8F CRC64;
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Query Match 85.2%; Score 3894; DB 2; Length 893;
Best Local Similarity 86.8%; Pred. No. 1.9e-242;
Matches 732; Conservative 25; Mismatches 68; Indels 18; Gaps 5;

QY 1 MSQTGSHPGRLAGRWGAQPCLLIPVPLSLVWLLLLLASLLPSARLASPLPREBE 60
Db 63 MSQMGHLPRGLTGHWRFPQCL-----PLHTVQWRRLLALLAFLSLAWPASPLPREBE 117
QY 61 IVFPEKLNG-SVLPGSGAPARLLCRLOAGTETLLLEQDSGVQVQVGLTVQYLGQAPELL 119
Db 118 IVFPEKLNGSSILPGSGVPARLLYRLPAFGEMLLLEQDPGVQVQVGLTVQYLGQAPELL 177
QY 120 GGAEPCTYLTGTINGDPESVASLHMDGGALLGLVQYRGAEHLHLPLEGGTPNSAGGFGAH 179
Db 178 GGAEPCTYLTGTINGDPESVASLHMDGGALLGLVQYRGAEHLHLPLEGGALNSAGGFGAH 237
QY 180 ILRRKSPASGQGMCMVKAPLSPSPRPRRAKRFASLSRFVETLVVADDKMAAFHAGLGLK 239
Db 238 ILRRKSPASGQGMCMVKAPLSPSPISRRTRKRFASLSRFVETLVVADDKMAAFHAGTGLK 297
QY 240 RYLLTVMAAAAKAFKHPISIRNPVSLVTVTRLVILSGEGEPQVG-----PSAAQTLSRFCA 294
Db 298 RYLLTVMAAAAKAFKHPISIRNPVSLVTVTRLVILSGEGEPQVG-----PSAAQTLSRFCA 353
QY 295 WORGMLTPSDSDPDHFDTAILFTRODLGCVSTCDTLGMADVGTVCDPARSCAIVEDDGLQ 354
Db 354 ---GASTPLTTQLITLTAILFTRODLGCVSTCDTLGMADVGTVCDPARSCAIVEDDGLQ 410
QY 355 SAFTAHAELGHVFNMLHDSKPCISLNGPLSTSRHVMAVMAHVDPEEPWSPCSARPTD 414
Db 411 SAFTAHAELGHVFNMLHDSKPCNTLNGQSSSRHVMAVMAHVDPEEPWSPCSARPTD 470
QY 415 FLNDNGYGHCLLDKPEAPLHLPVTFPGKYDADRCQCLTFGPDSSHCHCPQLPPCAALWCSC 474
Db 471 FLNDNGYGHCLLDKPEAPLHLPVTFPGKYDADRCQCLTFGPDSSHCHCPQLPPCAALWCSC 530
QY 475 HLNHAMCOTKHSFWADGTPCGPAQACMGGRCLHMDQLQDFNIPQAGGWPWGWDGDCSR 534
Db 531 HLNHAMCOTKHSFWADGTPCGSQAQCMGGRCLHVDQLQDFNVPQAGGWPWGWDGDCSR 590
QY 535 TCGGGVQFSSRDCTRPVPRNGGKYCEGRTFRSCNTDCTGTSALTFRBQCAAYNHR 594
Db 591 TCGGGVQFSSRDCTRPVPRNGGKYCEGRTFRSCNTDCTGTSALTFRBQCAAYNHR 650
QY 595 DLFKSPFGPMDWPRYTGVAPODCKLTCQARALGYVYVLEPRVVDGTPCSPDSSVVCVQ 654
Db 651 DLFKSPFGPMDWPRYTGVAPODCKLTCQARALGYVYVLEPRVVDGTPCSPDSSVVCVQ 710
QY 655 GRCIHAGCDRIIGSKKPKDKMVCGGDGGSGSKSGSPKRYGYNVVTIPAGATHILV 714
Db 711 GRCIHAGCDRIIGSKKPKDKMVCGGDGGSGSKSGSPKRYGYSVDVVTIPAGATHILV 770
QY 715 ROQGNPHRSYIALKLPDGSYALNGEYTLMPSPDVLPGAVSLRYSGATAASETLSGH 774
Db 771 ROQGGSGLSYIALKLPDGSYALNGEYTLMPSPDVLPGAVSLRYSGATAASETLSGH 830
QY 775 GPLAOPLTQLVLVAGNPQDTRLRYSFFVPRTPSTPRTPQDWLHRAQIILEILRRPWA 834
Db 831 GPLAOPLTQLVLVAGNPQARLRYSFFVPRVPTPRPPQDWLQRRABEILKLRKPWA 890
QY 835 GRK 837
Db 891 GRK 893

RESULT 8.
ID AC Q6A017;
DC 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE ADAMTS-4 precursor (BC 3.4.24.82) (A disintegrin and metalloproteinase
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EMBL; AB042272;	BAB16474.1;	-
EMBL; AB042271;	BAB16473.1;	-
EMBL; AB042273;	BAB16475.1;	-
HSPSP; P07996;	1LSL.	
MEROPS; M12.221;	-	
RGD; G21242;	Adamts4.	
InterPro; IPR010294;	ADAM_spacer1.	
InterPro; IPR001762;	Disintegrin.	
InterPro; IPR006025;	Pept_M_Zn_BS.	
InterPro; IPR001590;	Peptidase_M12B.	
InterPro; IPR000884;	TSP1.	
InterPro; IPR008085;	TSP 1.	
Pfam; PF05986;	ADAM_spacer1;	1.
Pfam; PF01421;	Reprolysin;	1.
Pfam; PF00090;	TSP_1;	1.
PRINTS; PR01705;	TSP1REPEAT.	
SMART; SM00209;	TSP1;	1.
PROSITE; PS0215;	ADAM_MEPRO;	1.
PROSITE; PS00427;	DISINTEGRIN_1;	FALSE_NEG.
PROSITE; PS0214;	DISINTEGRIN_2;	FALSE_NEG.
PROSITE; PS50092;	TSP1;	1.
PROSITE; PS00142;	ZINC_PROTEASE;	1.
KW Extracellular matrix;	Glycoprotein;	Hydrolase; Metalloprotease; Zinc;
KW Zymogen.		
FT NON TER	1	
FT PROPEP	<1	BY similarity.
FT CHAIN	6	ADAMTS-4.
FT DOMAIN	6	630 Metalloprotease.
FT DOMAIN	233	303 Disintegrin-like.
FT DOMAIN	313	368 TSP type-1.
FT DOMAIN	368	478 Cys-rich.

RESULT 9			
ID	ATS1_RAT	STANDARD	PRT; 967 AA.
AC	Q9WUQ1; Q9ER11;		
DT	16-OCT-2001 (Rel. 40, Created)		
DT	16-OCT-2001 (Rel. 40, Last sequence update)		
DT	25-OCT-2004 (Rel. 45, Last annotation update)		
DE	ADAMTS-1 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase with thrombospondin motifs 1) (ADAM-TS1) .		
GN	Name=Adamts1; Rat.		
OS	Rattus norvegicus (Rat.)		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus;		
OC	NCBI Taxid=10116;		

RESIT, T 9

RN SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Brain;
 RA Liu X., Tu Y., Yin T., Johnstone E.M., Stephenson D.T., Clemens J.A.,
 RA Little S.P.;
 RT "Induction of a disintegrin and metalloprotease with the
 RT thrombospondin type I motif (ADAMTS).";
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 [2]
 RN SEQUENCE OF 18-967 FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;
 RX MEDLINE=20304099; PubMed=10847486;
 RA Diamantis I., Luehli M., Hoesli M., Reichen J.;
 RT "Cloning of the rat ADAMTS-1 gene and its down regulation in
 RT endothelial cells in cirrhotic rats.";
 RL Liver 20:165-172(2000).
 CC -1- FUNCTION: Cleaves aggrecan, a cartilage proteoglycan, and may be
 CC involved in its turnover. Has angiogenic inhibitor activity (By
 CC similarity). Active metalloprotease, which may be associated with
 CC various inflammatory processes as well as development of cancer
 CC cachexia. May play a critical role in follicular rupture (By
 CC similarity).
 CC -1- CATALYTIC ACTIVITY: Cleaves aggrecan at the 1683-Glu-Leu-1684
 CC site, within the chondroitin sulfate attachment domain.
 CC -1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted. Associated with the extracellular
 CC matrix (By similarity).
 CC -1- INDUCTION: Down-regulated in endothelial cells derived from
 CC cirrhotic liver.
 CC -1- DOMAIN: The spacer domain and the TSP type-1 domains are important
 CC for a tight interaction with the extracellular matrix.
 CC -1- PTM: The precursor is cleaved by a furin endopeptidase (By
 CC similarity).
 CC -1- SIMILARITY: Belongs to the peptidase M12B family.
 CC -1- SIMILARITY: Contains 1 disintegrin-like domain.
 CC -1- SIMILARITY: Contains 3 TSP type-1 domains.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AF149118; AAD34012.1; -;
 DR EMBL: AF304446; AG29823.1; -;
 DR HSP: P07996; ILSL.
 DR MEROPS: M12.222; -;
 DR InterPro: IPR006586; ADAM_cysteine.
 DR InterPro: IPR010294; ADAM_spacer1.
 DR InterPro: IPR001762; Disintegrin.
 DR InterPro: IPR006025; Pept_M_Zn_BS.
 DR InterPro: IPR001590; Peptidase_M12B.
 DR InterPro: IPR002870; Peptidase_M12B_N.
 DR InterPro: IPR000884; TSP1.
 DR InterPro: IPR008085; TSP 1.
 DR Pfam: PF05986; ADAM_spacer1.
 DR Pfam: PF01562; Pep_M12B_propep; 1.
 DR Pfam: PF01421; Reprolysin; 1.
 DR Pfam: PF00090; TSP 1; 3.
 DR PRINTS: PR01705; TSP1REPEAT.
 DR SMART: SM00608; ACR; 1.
 DR SMART: SM00209; TSP1; 3.
 DR PROSITE: PS02015; ADAM_MEROPS; 1.
 DR PROSITE: PS00427; DISINTEGRIN 1; FALSE_NEG.
 DR PROSITE: PS02114; DISINTEGRIN 2; FALSE_NEG.
 DR PROSITE: PS00092; TSP1; 3.
 DR PROSITE: PS00142; ZINC_PROTEASE; 1.
 KW Extracellular matrix; Glycoprotein; Heparin-binding; Hydrolase;
 KW Metalloprotease; Repeat; Signal; Zinc; Zymogen.
 FT SIGNAL 1 54 Potential.
 FT PROPEP 55 252 By similarity.

FT CHAIN	253	967	ADAMTS-1.
FT DOMAIN	253	475	Metalloprotease.
FT DOMAIN	476	558	Disintegrin-like.
FT DOMAIN	559	614	TSP type-1 1.
FT DOMAIN	616	724	Cys-rich.
FT DOMAIN	725	857	Spacer.
FT DOMAIN	854	910	TSP type-1 2.
FT DOMAIN	911	967	TSP type-1 3.
FT DOMAIN	194	198	Poly-Arg.
FT SITE	205	205	Cysteine switch (Potential).
FT METAL	401	401	Zinc (catalytic) (By similarity).
FT ACT_SITE	401	402	By similarity.
FT METAL	405	405	Zinc (catalytic) (By similarity).
FT METAL	411	411	Zinc (catalytic) (By similarity).
FT CARBOHYD	547	547	N-linked (GlcNAc. .) (Potential).
FT CARBOHYD	720	720	N-linked (GlcNAc. .) (Potential).
FT CARBOHYD	764	764	N-linked (GlcNAc. .) (Potential).
FT CARBOHYD	782	782	N-linked (GlcNAc. .) (Potential).
FT CARBOHYD	945	945	N-linked (GlcNAc. .) (Potential).
FT CONFLICT	21	21	I -> V (in Ref. 2).
FT CONFLICT	26	31	KFRSQ -> RSRGL (in Ref. 2).
FT CONFLICT	49	49	V -> A (in Ref. 2).
FT CONFLICT	72	72	R -> P (in Ref. 2).
FT CONFLICT	79	79	L -> TR (in Ref. 2).
FT CONFLICT	249	249	R -> G (in Ref. 2).
FT CONFLICT	262	265	TMLV -> NLK (in Ref. 2).
FT CONFLICT	607	607	S -> F (in Ref. 2).
FT CONFLICT	936	936	L -> V (in Ref. 2).
FT CONFLICT	962	962	I -> T (in Ref. 2).
SQ SEQUENCE	967 AA;	105705 MW;	F93C864F6DCDB4CF CRC64;

Query Match 47.3%; Score 2161.5; DB 1; Length 967;
 Best Local Similarity 49.5%; Pred. No. 9.8e-131;
 Matches 415; Conservative 137; Mismatches 217; Indels 69; Gaps 16;

QY	37	LLLLLLAS--LPSARIA--SPLPRREEIVFPKINGSVLPGSGAPARLLCRLOAFQETL	92
Db	35	MLLLLLASITMLLCVRGAHGRPTDEELVLP-----SLERARGHDSLTLLRLDAFQQL	89
QY	93	LLELEODSGVQVGLTVQVGLQAPELLGGAEE-----PGTYLTGTINGDPESVASL	142
Db	90	HLKLQPSGFLAPGFTLTQTVGRSP-----GSEAHLDPDGLAHCFYSGTVNGDSSAAAL	145
QY	143	HWDDGALLGVLRGAELHLQP-----LEGGTP--NSAGGPGAHILRRKSPASQGP	192
Db	146	SLCEG-VRGAFYLGEEFFIQAPAVATERLVAEPKEESIAPRFHLRRRRGSG-GA	203
QY	193	MCNV-----KAPLGSPSP-----RPR-----RAKRFASLSRFVETL	223
Db	204	KCGVMEETLPTNSGREGSONTDQWPLRNPTQAGAKPTGPGSIRKKRFVSPRYVETM	263
QY	224	VVADDKMAAPHGAGLAKRYLLTVMAAAAKAFKPSIRNPVSLVTRVLVLGSGEGGPOVGP	283
Db	264	LVADQSMADPHGSLGKHYLLTLFSAARFYKHSIRNSISLVVVKILVIVYEQKGPVTS	323
QY	284	SAATLRSCAWQGLNTPEDSDPHDTAILTRQDLCGVSTCDTLGMADVGTVCDPAR	343
Db	324	NAALTNRFCSMQKHNSPSDRDPEHYDTAILTRQDLCGSHCTDLGMADVGTVCDPSR	383
QY	344	SCAIVEDDGLQSAFTAAHGLGHVFNMLHNSKPCISLNGPLSTSRHVMAVHVDPEEP	403
Db	384	SCSVIEDDGLQAAFTTAHGLGHVFNMPHDDAKHCASFNG-VSGDSHLMASMLSLDSHSQP	442
QY	404	WSPCSARFTDLDNGVGHCLLDKPEALHLPVTFPKDYDADRQCCLTGPDSRHCQP	463
Db	443	WSPCSAYMVTSLFDNGHGBCLMDKPNQPIKPSDLPTLYDANRQCQFTTGEESTHCPDA	502
QY	464	PPPCAALWCSGHLNGHAMCOTKHSPPWADGTPCCGPAQACMGCRCLHMDQLDQFNIPAGGW	523
Db	503	ASTCSTLWCTGTSGLLVLCQTKHFPWADGTSCEGKWCVSCKVNTDKHFAFPVHGSW	562
QY	524	GPWGPNGDCSRTCGGVQVFSRDCRTPVPVNGKYGCEGRTRFRSCNTEDCPTGSALTFR	583

Db 563 GPWPGWDCSRTCGGQVQYTMRECDNPVKNKGKCEGKRVYRSNIEDCPDNNKTFR 622
QY 584 EQCAAYNHRDILFKSPGPMQWVRYTGVAFODQCKLTQARALGYVYVLEPRVVDGTP 643
Db 623 EQCEAHNEFSKASFGNEPTVETPKYAGVSPKDRCKLTCEAKGIGYFVLPQPKVVDGTP 682
QY 644 CSPDSSVVCQRCIHAGCDRIIGSKKFKDKCMVCGDGGSGSKSGSPFRKFRYGNVNV 703
Db 683 CSPDSTSVCCQGVQVQVAGCDRIIGSKKFKDKCMVCGDGGSGSKSGSPFRKFRYGNVNV 742
QY 704 TIPAGATHILVROQGNPHRS--IYLALKLPDGSYALNGEYTIMSPSTVVLPGVSLRY 761
Db 743 TIPAGATNIEVKHNRPNRSGNNGSFLAIRAADGTYLNGNFTLSTLEQDLTYKGTV-LRY 801
QY 762 SGATASETLSGHGPLAQPLTLQVLVAGNPQDRLRYSPFVPRPT--PSTPRPTPDWL 818
Db 802 SGSSAALERIRSFPLKEPLTIQVLMVGHALRPKIKYTFMCKKTEFFNAITPFSWV 859

RESULT 10
Q68EJ2 PRELIMINARY; PRT; 967 AA.
AC Q68EJ2
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE A disintegrin and metalloproteinase with thrombospondin motifs 1.
GN Name=Adamtsl;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_taxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC PubMed12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuller G.D.,
RA Altchul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Director MGC Project;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC080237, AAH0237.1; -
DR GO, GO:0007229, P.integrin-mediated signaling pathway; IEA.
DR InterPro, IPR006586; ADAM cysteine.
DR InterPro, IPR010294; ADAM spacer1.
DR InterPro, IPR001590; Peptidase M12B.
DR InterPro, IPR002870; Peptidase M12B_N.
DR InterPro, IPR006025; Pept M_Zn_BS.
DR InterPro, IPR000884; TSP1.
DR InterPro, IPR008085; TSP1.
DR Pfam, PF05986; ADAM spacer1; 1.
DR Pfam, PF01562; Pep M12B propep; 1.
DR Pfam, PF01421; Repr0lysin; 1.

DR Pfam, PF00090; TSP_1; 3.
DR PRINTS, PR01705; TSP1REPEAT.
DR SMART, SMO0608; ACR; 1.
DR SMART, SMO0209; TSP1; 3.
DR PROSITE, PS02015; ADAM MEPRO; 1.
DR PROSITE, PS0092; TSP1; 3.
DR PROSITE, PS00143; ZINC_PROTEASE; UNKNOWN_1.
KW Integrin.
SQ SEQUENCE 967 AA; 105647 MW; C6349B5D8CBFEA24 CRC64;

Query Match 47.3%; Score 2160.5; DB 2; Length 967;
Best Local Similarity 49.5%; Pred. No. 1.1e-130;
Matches 415; Conservative 137; Mismatches 217; Indels 69; Gaps 16;

QY 37 LLLLLLAS--LLPSARLA--SPLPREBEIVPEPEKLNGSVLPFGCAPARLLCLRLQAFQETL 92
Db 35 MLLLLLASITMLLCVRGAHGRTBEDELVP-----SLERARGHGSTTLRLDAFGQOL 89
QY 93 LLELEODSGVQVEGLTVQYLQQAPELLGGAE-----PGTYLTGTGTINGDPEVSANSL 142
Db 90 HLKLPDSDGFLAPGFTLTQVGRSP-----GSEAQHLDPDGLAHCFYSGTVNGDPESSAAL 145
QY 143 HWDGALLGLVLYQYRAELHLP-----LEGTP--NSAGGPGAHILRRKSPASGQGP 192
Db 146 SLCEG--VRGAFYLOGEEFFIQPAPAVATERLVPAEPKEESTAPFRPHILRRRRSG-GA 203
QY 193 MCNV-----KAPLGSPSP-----RPR-----RAKRFASLRFVETL 223
Db 204 KCGVMEETLPTSNSGRESQNTPDQWFLRNPPOGAKPTGPGSIRKRRFVSSPRYVETM 263
QY 224 VVADDKMAAFHAGLKYLLTMAAAKAFKHPSTRNPVSLVTVLVLVLSGSEGPQVP 283
Db 264 LVADQSMADFHGSLKYLTLFSAARFYKHPSTRNSISLVVVKILYIEQKGPVETS 323
QY 284 SAAQTLRSCAWORGLNTPEDSDPDHEDTALLFTQDLGCVSTCTDLGMDVGTVCDPAR 343
Db 324 NAALTLRNFCWOKHNSPDRDPHYDTALLFTQDLGCVSTCTDLGMDVGTVCDPAR 383
QY 344 SCAIVEDDGLQSAFTAHELGHVFNMLHNSKPCISLNGPLTSRHHVMAVHVDPEEP 403
Db 384 SCSEIVEDDGLQAAFTTAHELGHVFNMPHDDAKHCASFNG--VSGDSHLMASMLSSLDHSP 442
QY 404 WSPCSARFTDLDNGYGHCLDKPEAPLHPVTPFGKDYDADROCOLTFFGDPDSRHCPQL 463
Db 443 WSPCSAYMTVSFLDNGHGECLMDKPNPILPSDLPTGLYDANRQCFIFGEESTHCPDA 502
QY 464 PPCCAALWCSHGLNHAMCQTHSPWADGTPCGPAQACMGRCCLHMDQLQODFNIPQAGW 523
Db 503 ASTCTSLNCTGTSGLLVQCQTHFPWADGTSCEGKVCVSGKCNKIDMKHFAIPVHGSW 562
QY 524 GPWPGWDCSRTCGGQVQVSSRDCTRPVPRNGKYCEGRTRFRSCNTEDCPTGSALTFR 593
Db 563 GPWPGWDCSRTCGGQVQVYTMRECDNPVKNKGKCEGKRVYRSNIEDCPDNNKTFR 622
QY 584 EQCAAYNHRDILFKSPGPMQWVRYTGVAFODQCKLTQARALGYVYVLEPRVVDGTP 643
Db 623 EQCEAHNEFSKASFGNEPTVETPKYAGVSPKDRCKLTCEAKGIGYFVLPQPKVVDGTP 682
QY 644 CSPDSSVVCQRCIHAGCDRIIGSKKFKDKCMVCGDGGSGSKSGSPFRKFRYGNVNV 703
Db 683 CSPDSTSVCCQGVQVQVAGCDRIIGSKKFKDKCMVCGDGGSGSKSGSPFRKFRYGNVNV 742
QY 704 TIPAGATHILVROQGNPHRS--IYLALKLPDGSYALNGEYTIMSPSTVVLPGVSLRY 761
Db 743 TIPAGATNIEVKHNRPNRSGNNGSFLAIRAADGTYLNGNFTLSTLEQDLTYKGTV-LRY 801
QY 762 SGATASETLSGHGPLAQPLTLQVLVAGNPQDRLRYSPFVPRPT--PSTPRPTPDWL 818
Db 802 SGSSAALERIRSFPLKEPLTIQVLMVGHALRPKIKYTFMCKKTEFFNAITPFSWV 859

RESULT 11
ATSL_MOUSE

ATSI_MOUSE STANDARD; PRT; 968 AA.
AC P97857; 054768;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE ADAMTS-1 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase
DE with thrombospondin motifs 1) (ADAM-TS 1) (ADAM-TS1).
GN Name=Adamts1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN=129/SVJ;
RC MEDLINE=98110583; PubMed=9441751; DOI=10.1006/geno.1997.5064;
RA Kuno K., Iizasa H., Ohno S., Matsushima K.;
RT "The exon/intron organization and chromosomal mapping of the mouse
RT ADAMTS-1 gene encoding an ADAM family protein with TSP motifs.";
RL Genomics 46:466-471(1997).
RN [2]
RN SEQUENCE FROM N.A.
RP MEDLINE=97150761; PubMed=8995297; DOI=10.1074/jbc.272.1.556;
RA Kuno K., Kanada N., Nakashima E., Fujiki F., Ichimura F.,
RA Matsushima K.;
RT "Molecular cloning of a gene encoding a new type of metalloproteinase-
RT disintegrin family protein with thrombospondin motifs as an
RT inflammation associated gene.";
RL J. Biol. Chem. 272:556-562(1997).
RN [3]
RN SEQUENCE FROM N.A.
RP TISSUE=Limb, and Mammary gland;
RC MEDLINE=2338257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Hopkins R.F., Jordan H., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Diatchenko L., Marusina K., Fawcett A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Bawa S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.T., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RN CHARACTERIZATION, AND MUTAGENESIS OF GLU-403.
RP MEDLINE=99303657; PubMed=10373500; DOI=10.1074/jbc.274.26.18821;
RA Kuno K., Terashima Y., Matsushima K.;
RT "ADAMTS-1 is an active metalloproteinase associated with the
RT extracellular matrix.";
RL J. Biol. Chem. 274:18821-18826(1999).
RN [5]
RN FUNCTION.
RP MEDLINE=20389568; PubMed=10930576; DOI=10.1016/S0014-5793(00)01854-8;
RA Kuno K., Okada Y., Kawashima H., Nakamura H., Miyasaka M., Ohno H.,
RA Matsushima K.;
RT "ADAMTS-1 cleaves a cartilage proteoglycan, aggrecan.";
RL FEBS Lett. 478:241-245(2000).
RN [6]
RN FUNCTION, AND INDUCTION.
RP MEDLINE=20243757; PubMed=10781075; DOI=10.1073/pnas.080073497;
RA Robker R.L., Russell D.L., Espey L.L., Lydon J.P., O'Malley B.W.,
RA Richards J.S.;
RT "Progesterone-regulated genes in the ovulation process: ADAMTS-1 and

cathepsin L proteases.";
Proc. Natl. Acad. Sci. U.S.A. 97:4689-4694(2000).
-!- FUNCTION: Cleaves aggrecan, a cartilage proteoglycan, and may be
involved in its turnover. Has angiogenic inhibitor activity (By
similarity). Active metalloproteinase, which may be associated with
various inflammatory processes as well as development of cancer
cachexia. May play a critical role in follicular rupture (By
similarity).
-!- CATALYTIC ACTIVITY: Cleaves aggrecan at the 1691-Glu-I-Leu-1692
site, within the chondroitin sulfate attachment domain.
-!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
-!- SUBCELLULAR LOCATION: Secreted. Associated with the extracellular
matrix.
-!- INDUCTION: Induced in vitro in colon adenocarcinoma cells by
interleukin-1, or in vivo in kidney and heart by
lipopolysaccharide. Also induced by LH stimulation in granulosa
cells of preovulatory follicles.
-!- DOMAIN: The spacer domain and the TSP type-1 domains are important
for a tight interaction with the extracellular matrix.
-!- PTM: The precursor is cleaved by a furin endopeptidase.
-!- SIMILARITY: Belongs to the peptidase M12B family.
-!- SIMILARITY: Contains 1 disintegrin-like domain.
-!- SIMILARITY: Contains 3 TSP type-1 domains.
-!- CAUTION: Ref.2 sequence differs from that shown due to a
frameshift in position 7.

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or send an email to license@sib-sib.ch).

EMBL; AB001735; BAA24501.1; ALT INIT.
EMBL; D67076; BAA11088.1; ALT_FRAME.
EMBL; BC040382; AAH40382.1; -.
EMBL; BC050834; AAH50834.1; -.
HSSP; P07996; 1LSL.
MEROPS; M12.222; -.
MGD; MGI:109249; Adamts1.
DR InterPro: IPR010294; ADAM_spacer1.
DR InterPro: IPR001762; Disintegrin.
DR InterPro: IPR006025; Pept_M_Zn_BS.
DR InterPro: IPR001590; Peptidase_M12B.
DR InterPro: IPR002870; Peptidase_M12B_N.
DR InterPro: IPR000884; TSP1.
DR InterPro: IPR008085; TSP_1.
DR Pfam: PF05986; ADAM_spacer1.1.
DR Pfam: PF01562; Pep_M12B_propep; 1.
DR Pfam: PF01421; Reprolysin; 1.
DR Pfam: PF00090; TSP_1; 3.
DR PRINTS; PR01705; TSP1REPEAT.
DR PROSITE; PS50215; ADAM_MEPRO; 1.
DR PROSITE; PS50427; DISINTEGRIN_1; FALSE NEG.
DR PROSITE; PS50214; DISINTEGRIN_2; FALSE NEG.
DR PROSITE; PS50092; TSP1; 3.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Extracellular matrix; Glycoprotein; Heparin-binding; Hydrolase;
FT Metalloproteinase; Repeat; Signal; Zinc; Zymogen.
FT SIGNAL 1 48 Potential.
FT PROPEP 49 253
FT CHAIN 254 968 ADAMTS-1.
FT DOMAIN 254 476 Metalloproteinase.
FT DOMAIN 477 559 Disintegrin-like.
FT DOMAIN 560 615 TSP type-1 1.
FT DOMAIN 618 725 Cys-rich.
FT DOMAIN 726 850 Spacer.
FT DOMAIN 855 911 TSP type-1 2.
FT DOMAIN 912 968 TSP type-1 3.
FT DOMAIN 195 199 Poly-Arg.
FT SITE 206 206 Cysteine switch (Potential).
FT METAL 402 402 Zinc (catalytic) (By similarity).

FT	ACT SITE	403		Zinc (catalytic) (By similarity).
FT	METAL	406		Zinc (catalytic) (By similarity).
FT	METAL	412		Zinc (catalytic) (By similarity).
FT	CARBOHYD	548		N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	721		N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	765		N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	783		N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	945		N-linked (GlcNAc. . .) (Potential).
FT	MUTAGEN	403		E->Q: Loss of activity.
FT	CONFLICT	335		N -> S (in Ref. 2).
FT	CONFLICT	425		T -> S (in Ref. 2).
SQ	SEQUENCE	968 AA;	428DA55499FB6C1	CRC64;
Query Match				
Best Local Similarity 49.4%; Pred. No. 1.7e-130;				
Matches 414; Conservative 135; Mismatches 221; Indels 68; Gaps 16;				
QY	37	LLLLLLAS--LLPSAKLA--SPLPREBEIVFPEKLSVLPFGSGAPARLLCRLQAFGETL	92	
DB	35	MLLLLLASITMLLCARGAHRTEDEELVPLSLERA---PGHDSQTTTL-RLDAFGQQL	90	
QY	93	LLELEQDSGVQVGLTVQYLGOAPELLGGAE-----PGTYLTGTINGDPESVASL	142	
DB	91	HLKLQPSGFLAFGLTQTVGRSP-----GSEAQLDPTGDLAHCFFYSGTVNGDPGSAAL	146	
QY	143	HWDCGALLGLVQYRGAEHLHQLLEG-----GTP--NSAGPGGAHLIRKSPASGQGP	192	
DB	147	SLCEG-VRGAFYLQGEFFIOPAPGVATERLAPVPEESSARPQPHILRRRRSGG-GA	204	
QY	193	MCNV-----KAPLGSPSRPR-----RAKRFASLSRFVETL	223	
DB	205	KCGVMDDETLPDSRPESQNTNRQWPVPTPODAGKPGSGIRKRVFSFVETM	264	
QY	224	VVADKMAAFHAGLKYLLTVMMAAAKAFKPSIRNPVSLVTVLRLVGLSGEGPQVGP	283	
DB	265	LVAQSQWADFSGGLKHYLLTLFVAARFYKPSIRNSISLVVVKILVYIEQKGPVTS	324	
QY	284	SAATLRSFCWQGLNTPESDDPHDFTALLFRQDLQGVSTCDTGMADVGTVCDDPAR	343	
DB	325	NAALTNRNFCWQKHSNPSRDEPHYDTALLFRQDLQGVSTCDTGMADVGTVCDDPSR	384	
QY	344	SCAIVDDGLQSAFTAAHELGHVFNMLHNSKPCISLNGPLSTSRHVMAFVMAHVDPEEP	403	
DB	385	SCSVIEDDLQQAFTAAHELGHVFNMPHDDAKHCSLNGVTGDS-HLWASMLSLDSQP	443	
QY	404	WSPCSARFITDNGYGHCLLDKPEAPLHLPVTFPGKYDADRCQCLTFGPDSSRHCPQL	463	
DB	444	WSPCSAYVWTSFLDNGHGECLMDKPNBPKLPSDLPLGTYDANRQCOQTFGSEKHCPEA	503	
QY	464	PPPCAALWCSHLNGHAMCOTKHSFPAWGTGCPGAQACWGGRCGLHMDLODFNIPQAGGW	523	
DB	504	ASTCTTLMCTGTSGLLVCQTKHFPWADGTCGEGKWCVCGRKCNKTKDKHFAFVHGSW	563	
QY	524	GPWGPWGDSCRTCGGGVQVSSRDCTRPVPRNGKTCYCEGRTRFRSCNTEDCPTGSALTFR	583	
DB	564	GPWGPWGDSCRTCGGGVQVWYMECDNPPVKGKTCYCEGRTRFRSCNTEDCPTGSALTFR	623	
QY	584	EQCCAAVNRHRLDFKSPGPMWVRYTGVAPQDCKLTQCARALGYVYVLEPRVVDGTP	643	
DB	624	EQCCAAHNEFSAKSPGNEPTWETPKYAGVSPKDRCKLTCEAKGIGYFVLPQKVVDTGP	683	
QY	644	CSPDSSVCQGRCHTAGCDRIIGSKKFKDKWCVGGGSGKSGKSGFRKFRFYGNVNV	703	
DB	684	CSPDSTSVCCQGVKAGCDRIIDSKKFKDKGCVGGSGSTCKKWSGIVTSTRPGYHDIV	743	
QY	704	TIPAGATHILVRQGNPHGRS--IYIALKLPDGSVALNGEYTLMPSTVTLPGVSLRY	761	
DB	744	TIPAGATNIEVXHRNQGRNNGSFLAIRAADGTVTLNGNFTLSTLEQDLTYKGTV-LRY	802	
QY	762	SGATASETLSHGFLAQLTQVLVAGNPQDTRLRYSPFVPRTPS-TPRTPDQWL	818	
DB	803	SGSSAALIRSPSPLEKPLTIQVLMVGHALRPKIKFTYFMKKTKTESFWAITFSEW	860	

RESULT 12				
ID	ATSI_HUMAN	STANDARD;	PRT;	967 AA.
AC	Q9UHI8; Q9NSJ8; Q9P2K0; Q9U8H3; Q9UP80;			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	ADAMTS-1 precursor (BC 3.4.24.-) (A disintegrin and metalloproteinase			
DE	with thrombospondin motifs 1) (ADAM-TS 1) (ADAM-TS1) (METH-1).			
GN	Name=ADAMTS1; Synonyms=KIAA1346, METH1;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_taxid=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Casas C., Pritchard M.A., Estivill X., Arbones M.L.;			
RT	"Cloning, characterization and mapping on human chromosome 21 of the			
RT	orthologue of murine Adamts-1.;"			
RL	Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A., AND FUNCTION.			
RC	TISSUE=Heart;			
RX	MEDLINE=99367466; PubMed=10438512; DOI=10.1074/jbc.274.33.23349;			
RA	Vazquez F., Hastings G., Ortega M.A., Lane T.F., Oikemus S.,			
RA	Lombardo M., Iruela-Arispe M.L.;			
RT	"METH-1, a human orthologue of ADAMTS-1, and METH-2 are members of a new			
RT	family of proteins with angio-inhibitory activity.;"			
RL	J. Biol. Chem. 274:23349-23357(1999).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Endothelial cells;			
RX	MEDLINE=20247184; PubMed=10785405;			
RA	Glienke J., Schmitt A.O., Pillarsky C., Hinzmann B., Weiss B.,			
RA	Rosenthal A., Thierach K.H.;			
RT	"Differential gene expression by endothelial cells in distinct			
RT	angiogenic states.;"			
RL	Eur. J. Biochem. 267:2820-2830(2000).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RX	MEDLINE=20181126; PubMed=10718198;			
RA	Nagase T., Kikuno R., Ishikawa K.-I., Hirose M., Ohara O.;			
RT	"Prediction of the coding sequences of unidentified human genes. XVI.			
RT	The complete sequences of 150 new cDNA clones from brain which code			
RT	for large proteins in vitro.;"			
RL	DNA Res. 7:65-73(2000).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RC	MEDLINE=20289799; PubMed=10830953; DOI=10.1038/35012518;			
RA	Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,			
RA	Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Soeda E.,			
RA	Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K., Polley A.,			
RA	Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,			
RA	Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,			
RA	Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,			
RA	Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,			
RA	Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandt P.,			
RA	Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Blocker H.,			
RA	Ranger J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.,			
RA	Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,			
RA	Lehrach H., Reinhardt R., Yaspo M.-L.;			
RT	"The DNA sequence of human chromosome 21.;"			
RL	Nature 405:311-319(2000).			
RN	[6]			
RP	SEQUENCE OF 418-967 FROM N.A.			
RC	TISSUE=Melanoma;			
RA	Blum H., Baurasachs S., Mewes H.-W., Weil B., Wiemann S.;			
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.			
CC	!- FUNCTION: Cleaves aggrecan, a cartilage proteoglycan, and may be			
CC	involved in its turnover (By similarity). Has angiogenic inhibitor			
CC	activity. Active metalloprotease, which may be associated with			

various inflammatory processes as well as development of cancer cachexia. May play a critical role in follicular rupture.

-1- CATALYTIC ACTIVITY: Cleaves aggrecan at the 1938-Glu-|-Leu-1939 site, within the chondroitin sulfate attachment domain.

-1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).

-1- SUBCELLULAR LOCATION: Secreted. Associated with the extracellular matrix (By similarity).

-1- DOMAIN: The spacer domain and the TSP type-1 domains are important for a tight interaction with the extracellular matrix.

-1- PTM: The precursor is cleaved by a furin endopeptidase (By similarity).

-1- SIMILARITY: Belongs to the peptidase M12B family.

-1- SIMILARITY: Contains 1 disintegrin-like domain.

-1- SIMILARITY: Contains 3 TSP type-1 domains.

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DR EMBL; AF170084; AAF15317.1; -. ALT_INIT.

DR EMBL; AF060152; AAD48080.1; -. ALT_INIT.

DR EMBL; AF207664; AAF23772.1; -. ALT_INIT.

DR EMBL; AB037767; BAA92584.1; -. ALT_INIT.

DR EMBL; AP001697; BAA95502.1; -. ALT_INIT.

DR EMBL; AL162080; CAB82413.1; -. ALT_INIT.

DR EMBL; T47158; T47158.

DR HSSP; P07996; 1LSL.

DR MEROPS; M12.222; -. Genew; HGNC:217; ADAMTS1.

DR H-InvDB; HIX0016042; -. MIM; 605174; -. GO; GO:0008237; F:metallopeptidase activity; TAS.

DR GO; GO:0007229; P:integrin-mediated signaling pathway; TAS.

DR GO; GO:0008285; P:negative regulation of cell proliferation; TAS.

DR InterPro; IPR006586; ADAM cysteine.

DR InterPro; IPR010294; ADAM_spacer1.

DR InterPro; IPR001762; Disintegrin.

DR InterPro; IPR001590; Peptidase M12B.

DR InterPro; IPR002870; Peptidase M12B_N.

DR InterPro; IPR006025; Pept M_Zn_BS.

DR InterPro; IPR000884; TSP1.

DR InterPro; IPR008085; TSP1.

DR Pfam; PF05986; ADAM_spacer1; 1.

DR Pfam; PF01562; Pep_M12B_propept; 1.

DR Pfam; PF01421; Reprolysin; 1.

DR Pfam; PF00090; TSP_1; 3.

DR PRINTS; PR01705; TSP1REPEAT.

DR SMART; SM00508; ACR; 1.

DR SMART; SM00209; TSP1; 3.

DR PROSITE; PS00215; ADAM_MEPRO; 1.

DR PROSITE; PS00427; DISINTEGRIN_1; FALSE_NEG.

DR PROSITE; PS00214; DISINTEGRIN_2; FALSE_NEG.

DR PROSITE; PS00092; TSP1; 3.

DR PROSITE; PS00142; ZINC_PROTEASE; 1.

KW Extracellular matrix; Glycoprotein; Heparin-binding; Hydrolase;

KW Metalloprotease; Repeat; Signal; Zinc; Zymogen.

FT SIGNAL 1 49 Potential.

FT PROPEP 50 252 By similarity.

FT CHAIN 253 967 ADAMTS-1.

FT DOMAIN 253 475 Metalloprotease.

FT DOMAIN 476 559 Disintegrin-like.

FT DOMAIN 559 614 TSP type-1.

FT DOMAIN 617 724 Cys-rich.

FT DOMAIN 725 849 Spacer.

FT DOMAIN 854 905 TSP type-1 2.

FT DOMAIN 908 967 TSP type-1 3.

FT DOMAIN 983 846 Poly-lys.

FT SITE 198 198 Cysteine switch (Potential).

FT METAL 401 401 Zinc (catalytic) (By similarity).

FT	ACT SITE	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	524	525	526	527	528	529	530	531	532	533	534	535	536	537	538	539	540	541	542	543	544	545	546	547	548	549	550	551	552	553	554	555	556	557	558	559	560	561	562	563	564	565	566	567	568	569	570	571	572	573	574	575	576	577	578	579	580	581	582	583	584	585	586	587	588	589	590	591	592	593	594	595	596	597	598	599	600	601	602	603	604	605	606	607	608	609	610	611	612	613	614	615	616	617	618	619	620	621	622	623	624	625	626	627	628	629	630	631	632	633	634	635	636	637	638	639	640	641	642	643	644	645	646	647	648	649	650	651	652	653	654	655	656	657	658	659	660	661	662	663	664	665	666	667	668	669	670	671	672	673	674	675	676	677	678	679	680	681	682	683	684	685	686	687	688	689	690	691	692	693	694	695	696	697	698	699	700	701	702	703	704	705	706	707	708	709	710	711	712	713	714	715	716	717	718	719	720	721	722	723	724	725	726	727	728	729	730	731	732	733	734	735	736	737	738	739	740	741	742	743	744	745	746	747	748	749	750	751	752	753	754	755	756	757	758	759	760	761	762	763	764	765	766	767	768	769	770	771	772	773	774	775	776	777	778	779	780	781	782	783	784	785	786	787	788	789	790	791	792	793	794	795	796	797	798	799	800	801	802	803	804	805	806	807	808	809	810	811	812	813	814	815	816	817	818	819	820	821	822	823	824	825	826	827	828	829	830	831	832	833	834	835	836	837	838	839	840	841	842	843	844	845	846	847	848	849	850	851	852	853	854	855	856	857	858	859	860	861	862	863	864	865	866	867	868	869	870	871	872	873	874	875	876	877	878	879	880	881	882	883	884	885	886	887	888	889	890	891	892	893	894	895	896	897	898	899	900	901	902	903	904	905	906	907	908	909	910	911	912	913	914	915	916	917	918	919	920	921	922	923	924	925	926	927	928	929	930	931	932	933	934	935	936	937	938	939	940	941	942	943	944	945	946	947	948	949	950	951	952	953	954	955	956	957	958	959	960	961	962	963	964	965	966	967	968	969	970	971	972	973	974	975	976	977	978	979	980	981	982	983	984	985	986	987	988	989	990	991	992	993	994	995	996	997	998	999	1000
FT	METAL	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	524	525	526	527	528	529	530	531	532	533	534	535	536	537	538	539	540	541	542	543	544	545	546	547	548	549	550	551	552	553	554	555	556	557	558	559	560	561	562	563	564	565	566	567	568	569	570	571	572	573	574	575	576	577	578	579	580	581	582	583	584	585	586	587	588	589	590	591	592	593	594	595	596	597	598	599	600	601	602	603	604	605	606	607	608	609	610	611	612	613	614	615	616	617	618	619	620	621	622	623	624	625	626	627	628	629	630	631	632	633	634	635	636	637	638	639	640	641	642	643	644	645	646	647	648	649	650	651	652	653	654	655	656	657	658	659	660	661	662	663	664	665	666	667	668	669	670	671	672	673	674	675	676	677	678	679	680	681	682	683	684	685	686	687	688	689	690	691	692	693	694	695	696	697	698	699	700	701	702	703	704	705	706	707	708	709	710	711	712	713	714	715	716	717	718	719	720	721	722	723	724	725	726	727	728	729	730	731	732	733	734	735	736	737	738	739	740	741	742	743	744	745	746	747	748	749	750	751	752	753	754	755	756	757	758	759	760	761	762	763	764	765	766	767	768	769	770	771	772	773	774	775	776	777	778	779	780	781	782	783	784	785	786	787	788	789	790	791	792	793	794	795	796	797	798	799	800	801	802	803	804	805	806	807	808	809	810	811	812	813	814	815	816	817	818	819	820	821	822	823	824	825	826	827	828	829	830	831	832	833	834	835	836	837	838	839	840	841	842	843	844	845	846	847	848	849	850	851	852	853	854	855	856	857	858	859	860	861	862	863	864	865	866	867	868	869	870	871	872	873	874	875	876	877	878	879	880	881	882	883	884	885	886	887	888	889	890	891	892	893	894	895	896	897	898	899	900	901	902	903	904	905	906	907	908	909	910	911	912	913	914	915	916	917	918	919	920	921	922	923	924	925	926	927	928	929	930	931	932	933	934	935	936	937	938	939	940	941	942	943	944	945	946	947	948	949	950	951	952	953	954	955	956	957	958	959	960	961	962	963	964	965	966	967	968	969	970	971	972	973	974	975																									

Q8NE26	PRELIMINARY;	PRT;	967 AA.
AC	Q8NE26;		
DT	01-OCT-2002 (T-EMBLrel. 22, Created)		
DT	01-OCT-2002 (T-EMBLrel. 22, Last sequence update)		
DT	01-MAR-2004 (T-EMBLrel. 26, Last annotation update)		
DE	A disintegrin and metalloprotease with thrombospondin motifs-1,		
DE	preproprotein.		
GN	Name=ADAMTS1;		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Testis;		
RC	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;		
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,		
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,		
RA	Diatchenko L., Narusina K., Farmer A.A., Rubin G.M., Hong L.,		
RA	Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,		
RA	Brownstein M.J., Udell T.B., Toshyuki S., Carninci P., Prange C.,		
RA	Raha S.S., McQuellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,		
RA	Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
RA	Richards S., Wozley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,		
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	Faney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,		
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,		
RA	Krzywinski M.I., Skalska U., Smalusz D.B., Schnerch A., Schein J.E.,		
RA	Jones S.J., Marra M.A.;		
RT	"Generation and initial analysis of more than 15,000 full-length human		
RT	and mouse cDNA sequences."		
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Testis;		
RA	Director MGC Project;		
RL	Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; BC036515; AAH36515.1; -		
DR	HSSP; P07996; ILSU.		
DR	GO; GO:0004223; F:metalloendopeptidase activity; IEA.		
DR	GO; GO:0007223; P:integrin-mediated signaling pathway; IEA.		
DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.		
DR	InterPro; IPR006586; ADAM_cysteine.		
DR	InterPro; IPR010294; ADAM_spacer1.		
DR	InterPro; IPR001128; Cytochrome P450.		
DR	InterPro; IPR001590; Peptidase_M12B.		
DR	InterPro; IPR002870; Peptidase_M12B_N.		
DR	InterPro; IPR006025; Pept_M_Zn_BS.		
DR	InterPro; IPR000884; TSP1.		
DR	InterPro; IPR008085; TSP 1.		
DR	Pfam; PF05986; ADAM_spacer1.1.		
DR	Pfam; PF01562; Pep_M12B_propep.1.		
DR	Pfam; PF01421; Reprolysin; 1.		
DR	Pfam; PF00090; TSP 1; 3.		
DR	PRINTS; PR01705; TSP1REPEAT.		
DR	SMART; SM00608; ACR; 1.		
DR	SMART; SM00209; TSP1; 3.		
DR	PROSITE; PS00215; ADAM_MEPRO; 1.		
DR	PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.		
DR	PROSITE; PS00092; TSP1; 3.		
DR	PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.		
KW	Integrin; Metalloprotease; Protease.		
SQ	SEQUENCE 967 AA; 105387 MW; FFID399674201C3D CRC64;		

Query Match. 46.5%; Score 2127; DB 2; Length 967;

Best Local Similarity 49.4%; Pred. No. 1.6e-128;

Matches 414; Conservative 127; Mismatches 227; Indels 70; Gaps 18;

QY	37	LLLLLLASLLPSARLASPLPREBEIVPEPKLNGSVLPFGCAPARLLCRLOAFGETLLEL	96
DB	36	LLLLAAALLAVSDALGRPSEDEELVPELERA---PGHGT--TRL--RLHAFDQDLDEL	89
QY	97	EQDSGVQVEGLTVQYLQAPPELLGGAB---PGT-----YLTGTINGDPESVASLHWDGGA	148
DB	90	RPDSSFLAPGFTLQNVGRK-----SGSETPLPETDLAHCFFSYGVNGDPSSAALSCEG-	144
QY	149	LLGVLYRGAEHLHQLPLEGGTPNSA-CGPGA-----HILRRK-----	184
DB	145	VRGAFYLLGEAYFTIQLPAASERLATAAPGEKPPAPLQFHLRLNRRODVGTCGVVDDE	204
QY	185	-----SPASGGQCMNVKAP-----LGSFSPRPR-RAKRFASLSRFVETLV	224
DB	205	PRPTGKAETDEDESGTEGEDEGPQWSPQDPALQGVQPTGTGTSIRKRFVSSHRYVETML	264
QY	225	VADKMAAFHAGLKYRYLLTVMAAAAKAFKHPSTRNPVSLVTVTLVILGSGEEGPQVGPS	284
DB	265	VADQSMABFHGSLKHYLLTLFSAARLYKHPSTRNSVSLVVVILVHDEQKGPVTSN	324
QY	285	AAQTLSFCANQRLNTPEDSDPDHFDTAILFTQDLGCGVSTCDTLGMADVGTVCDPARS	344
DB	325	AALTURNFNNQKQINPSPDRDAEHYDAILFTQDLGCGVSTCDTLGMADVGTVCDPARS	384
QY	345	CAIVEDDGLQSAFTAHAHELGVFNMLHNSKPCISLNGPLSTRHVPVMAVMAHVDPPEPW	404
DB	385	CSVIEDDGLQAAFTTAHELGHVFNMPHDDAKQCASLNG-VNQDSHMMASMLSNLDHSPW	443
QY	405	SPCSARFTFDLDNGYGHCLDKPEAPLHLPVTPPGKYDADROCOLTFPGDPSRHCPQLP	464
DB	444	SPCSAYMTITSFLDNGHGECLMDKPNQIQLPDLPTGTSYDANRQCQFTFGEDSKHCPDAA	503
QY	465	PPCAALWCSHGLNHGAMQTKHSPWADGTPCPAPAAQCMGRCGLHMDQLQDNPIPAQGWG	524
DB	504	STCSTLWCTGTSGGVLVQCTKHFWADGTSCEGKWCINGKCVNKTDRKHFTPTPHGSMG	563
QY	525	PMGPMGDCSRTCGGVQFSSRDCRTPVPRNGKCYCEGRTRFRSCNTEBDCPTGSAITFRE	584
DB	564	MMGPMGDCSRTCGGVQVYTRCDNPNPKNGKCYCEGRKRVYRSCNLEDCPDNNGKTFRE	623
QY	585	EQCAAYNHRTDL-FKSFPGPMDWVRYTGVAPODQCKLTQCARALGYVYVLEPRVVDGTP	643
DB	624	EQCEAHNEFSKASFGSGPA-VEMI PKYAGVSPKDRCKLICQAKGIGYFFVLQPKVVDGTP	682
QY	644	CSPDSSVVCQGRCHAGCDRIIGSKKFDKCMWCGDGGSCGSGSGSKGSKFRERYGVNVV	703
DB	683	CSTDSTSVCCQGVKAGCDRIIDSKKFDKCMWCGDGGSGSGSGSKGSKFRERYGVNVV	742
QY	704	TIPAGATHILVRQGNPHRS--IYLALKLPDGSVALNGEYTLMPSPDTDVILPFGAVSLRY	761
DB	743	TIPTGATNIEVKORNGSRNNGSFLAIKAADGYTLNGDYTLSTLEQDIMYGVV-LRY	801
QY	762	SGATAASETLGSHGGLAQPLTLQVLVAGNPQDTRLYSFFVRPPTS-TPRPTPDWL	818
DB	802	SGSSAALERIRSPSPLKEPLTIQVLTVGNALRPKIKYTYFVKKKKESFNAIPTFSAW	859

RESULT 14

Q8H2M8	PRELIMINARY;	PRT;	759 AA.
AC	Q8H2M8;		
DT	01-MAR-2003 (T-EMBLrel. 23, Created)		
DT	01-MAR-2003 (T-EMBLrel. 23, Last sequence update)		
DT	01-MAR-2004 (T-EMBLrel. 26, Last annotation update)		
DE	Metalloprotease (fragment).		
GN	Name=ADAMTS-1;		
OS	Equus caballus (Horse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Perissodactyla; Equidae; Equus.		
OX	NCBI_TaxID=9796;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Boerboom D., Russell D.L., Richards J.S., Sirois J.;		

Db 637 KXESFNAIPTFSEWV 651

RESULT 15

AT15_HUMAN

ID - AT15_HUMAN STANDARD; PRT; 950 AA.

AC Q8TE56;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE ADAMTS-15 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase with thrombospondin motifs 15) (ADAM-TS 15) (ADAM-TS15).

GN Name=ADAMTS15;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

XX [1]

RN SEQUENCE FROM N.A.

RP MDLINE=21856482; PubMed=11867212; DOI=10.1016/S0378-1119(01)00861-7;

RX Cal S., Obaya A.J., Llamazares M., Garabaya C., Quesada V., RA Lopez-Otin C.;

RA "Cloning, expression analysis, and structural characterization of RT seven novel human ADAMTS, a family of metalloproteinases with RT disintegrin and thrombospondin-1 domains";

RL Gene 283:49-62(2002).

CC -1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).

CC -1- SUBCELLULAR LOCATION: Secreted. Associated with the extracellular matrix (By similarity).

CC -1- TISSUE SPECIFICITY: Expressed in fetal liver and kidney, but not in any of the adult tissues examined.

CC -1- DOMAIN: The spacer domain and the TSP type-1 domains are important for a tight interaction with the extracellular matrix (By similarity).

CC -1- FMW: The precursor is cleaved by a furin endopeptidase (By similarity).

CC -1- SIMILARITY: Belongs to the peptidase M12B family.

CC -1- SIMILARITY: Contains 1 disintegrin-like domain.

CC -1- SIMILARITY: Contains 3 TSP type-1 domains.

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CC -----

DR EMBL: AJ315733; CAC86014.1; -.

DR HSSP: P07996; 1L5L.

DR MEROPS: M12.025; -.

DR Genew; HGNC:16305; ADAMTS15.

DR MIM; 607509; -.

DR InterPro; IPR010294; ADAM_spacer1.

DR InterPro; IPR001762; Disintegrin.

DR InterPro; IPR001590; Peptidase_M12B.

DR InterPro; IPR002870; Peptidase_M12B_N.

DR InterPro; IPR01818; Pept_M10A_M12B.

DR InterPro; IPR006025; Pept_M_Zn_BS.

DR InterPro; IPR000884; TSP1.

DR Pfam; PF05986; ADAM_spacer1; 1.

DR Pfam; PF01562; Pep_M12B_propep; 1.

DR Pfam; PF01421; Reprolysin; 1.

DR Pfam; PF00090; TSP_1; 3.

DR SMART; SM00209; TSP1; 3.

DR PROSITE; PS00215; ADAM_MEPPO; 1.

DR PROSITE; PS00546; CYSTEINE_SWITCH; FALSE_NEG.

DR PROSITE; PS00427; DISINTEGRIN_1; FALSE_NEG.

DR PROSITE; PS00214; DISINTEGRIN_2; FALSE_NEG.

DR PROSITE; PS00092; TSP1; 3.

DR PROSITE; PS00142; ZINC_PROTEASE; 1.

KW Extracellular matrix; Glycoprotein; Hydrolase; Metalloprotease;

Qy 716 QQNGPG--HRSIYLALKLPDGSYALNGEYTLMPSTDDVLPGLVAVSLRYSGATAASETLSG 773
Db 713 QRGYKGLIGDDNYLALKNSOGKYLINGHFVVSAVERDLVVKGL-LRYSGTGTAVESLQA 771
Qy 774 HGPLAQPLTLQVLVAGNPQDTRLRYSFFVPRPTPTSTPRTPQD 816
Db 772 SRFILEPLTVEVLVSGKWTTPRVRYSPFLPKPEPREDKSSHPKD 814

Search completed: April 1, 2005, 12:51:40
Job time : 192 secs

KW Repeat; Signal; Zinc; Zymogen. Potential.
FT SIGNAL 1 17
FT PROPEP 18 212 By similarity.
FT CHAIN 213 950 ADAMS-15.
FT DOMAIN 213 427 Metalloprotease.
FT DOMAIN 428 515 Disintegrin-like.
FT DOMAIN 516 571 TSP type-1 1.
FT DOMAIN 572 700 Cys-rich.
FT DOMAIN 701 838 Spacer.
FT DOMAIN 839 895 TSP type-1 2.
FT DOMAIN 896 949 TSP type-1 3.
FT SITE 174 174 Cysteine switch (Potential).
FT METAL 361 361 Zinc (catalytic) (By similarity).
FT ACT SITE 362 362 By similarity.
FT METAL 371 371 Zinc (catalytic) (By similarity).
FT METAL 371 371 Zinc (catalytic) (By similarity).
FT CARBOHYD 141 141 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 591 591 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 623 623 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 679 679 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 950 AA; 103286 MW; 5DFBE18285CCCC3B CRC64;

Query Match 41.9%; Score 1915; DB 1; Length 950;
Best Local Similarity 46.3%; Pred. No. 7.4e-115; Indels 52; Gaps 16;
Matches 381; Conservative 123; Mismatches 267;

Qy 37 LLLLLASLLPSARLASPLPREBEIVPEKINGSVL-----PGSGAPARLLCRLOAF 88
Db 1 MLLGLITLAPAGTAGGSEPEREVVPIRLDPDINGRRYVRGPEDSGQGLIFQITAF 60
Qy 89 GETLLLEQDSGVQVGLTVQYLGQAPL-LGGAEP--GTYLTGTINGDPESVASLHWD 145
Db 61 QEDFYHLTPDAQPLAPAFSTHGLVPLQGLTGGSDLRRCFYSGDVNAEPDSPAVALSC 120
Qy 146 GGALLGVLYQGAELHQLPLEGGTPNSA--GGCAHILRRK---SPASQCGPMCNV--- 196
Db 121 GG-LRGAFYRGAEYVISPLENASAPAAQRNSQAHLLQRRGVPGGPGDPTSRGCVASG 179
Qy 197 -----KAPLGSPPRPR--RAKRFASLSRFVETLVVADDDMAAFHGAGLK 239
Db 180 WNPAILRALDPYKPRRAGFGESRRRSRRAKRFVSIPIRYVETLVVADESVMVFPHGADLE 239
Qy 240 RYLLITVMAAARAKFKPSIRNPVSLVTVTLVILSGEGEPQVPSAAQTILRSFCAMQRL 299
Db 240 HYLTLTATAARLYRHSILPNIPIVVKVLLLRDRSGFKVTGNALTLLENFCAMQKL 299
Qy 300 NTPEDSDPHFDFTALFTRQDLGVSTCDTILGMADVGTVCDDPARSCAIVEDDGLQSAFTA 359
Db 300 NKVSKHPEYWDTALFTTRQDLCGATTCDTLGMADVGTMCDDPKRSCSVIEDDGLPSAFTT 359
Qy 360 AHELGHVFNMLHDNSKPCISLNGPLSTSRHVMAPVMAHVDPPEEPWSPCSARFITDFLDNG 419
Db 360 AHELGHVFNMLHDNSKPCISLNGPLSTSRHVMAPVMAHVDPPEEPWSPCSARFITDFLDNG 418
Qy 420 YGHCLLDKPEAPLHPVFPFGDYDADRCQQLTFGDSRHCPQLPFPCCALWCSEHLNGH 479
Db 419 HGDCLLDQPSKFIISLPEDLPAGSYTLQQCELAFGVSGKPCPYM-QYCTKLWCTGKAKGQ 477
Qy 480 AMCQTKHSPWADGTPCGPAQACMGRCCLHMDQLQDNIPQAGGWPWGPGWDCSRTCGG 539
Db 478 MVCQTRHPFWADGTSCEGKCLKACVVERHNLKHRVD--GSWAKWDPYGPCSRTCGG 535
Qy 540 VQFSSRDCTRPVRNGGKYCEGRRTRFRSCNTDCP-TGSALTFRREQCAA---YNNRTD 595
Db 536 VQLARRQCTNPTFANGGKYCEGVVRKYRSCNLEPCPSSASGKSFREEQCEAFNGYNHSTN 595
Qy 596 LFKSFPFGMDWPRYTGVAPOCKLITCOARALGYYYVLEPRVVDGTPCSPDSSSVCVQG 655
Db 596 RLTL---AVAWPKYSGVSPDKCLICRANGTYFYVLAPKVDGTLCSPDSTSVCVQG 652
Qy 656 RCHACDRIIGSKKFKDKMVGCGSGCSKOSKFRKFRGYNNVVTIPAGATHILVR 715
Db 653 KCIKAGCDGNLGSKKRFDKCGVCGGDNKSKCKVTGLTKPMHGYNFVVAIPAGASSIDIR 712